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(54) **IMMUNODOMINANT HUMAN T-CELL EPITOPES OF HEPATITIS C VIRUS**

VON MENSCHLICHEN T-ZELLEN IMMUNODOMINANTE EPIROPEN DES VIRUS DER  
C-HEPATITIS

EPITOPES DE LYMPHOCYTES T HUMAINS IMMUNODOMINANTS DU VIRUS DE L'HEPATITE C

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(74) Representative: **De Clercq, Ann  
De Clercq, Brants & Partners cv.,  
Edgard Gevaertdreef 10a  
9830 Sint-Martens-Latem (BE)**

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(73) Proprietor: **INNOGENETICS N.V.  
9052 Ghent (BE)**

(72) Inventors:  
• **LEROUX-ROELS, Geert  
B-9000 Ghent (BE)**  
• **DELEYS, Robert  
B-1850 Grimbergen (BE)**  
• **MAERTENS, Geert  
B-8310 Brugge (BE)**

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- **JOURNAL OF VIROLOGY**, vol.67, no.12, December 1993 pages 7522 - 7532 KOZIEL, M. J. ET AL. 'Hepatitis C Virus (HCV)-specific cytotoxic T lymphocytes recognize epitopes in the core and envelope proteins of HCV'

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**Description**

**[0001]** The present invention describes immunodominant hepatitis C virus T cell epitopes useful in hepatitis C prophylactic and therapeutic vaccines, derived from the HCV core, protein.

Technical field of the invention

**[0002]** The present invention relates to the production of novel synthetic immunogens related to the hepatitis C virus core region and to the use thereof in the production of vaccines, therapeutic agents and the like. More specifically, the present invention relates to polypeptide compositions containing HCV core, T cell determinants.

Background of the invention

**[0003]** In the few years since its discovery, Hepatitis C virus (HCV) has been shown to be a major cause of acute and chronic liver disease. HCV is a single-stranded RNA virus with a genome of approximately 9400 nucleotides that consists of a 5' untranslated region (5'UR) of 341 nucleotides which precedes a single large open reading frame encoding a precursor polypeptide of about 3010 amino acids (Kato et al., 1990). The genetic organization of the viral genome is related to that of flavi- and pestiviruses, with the putative structural proteins located in the N-terminal region and a variety of non structural proteins located at the C-terminal end of the polypeptide. The structural proteins are the core protein (C, amino acids 1-191) followed by the putative envelope proteins E1 (amino acids 192-383) and E2/NS1 (amino acids 384-746). The terms E2 and NS1 are often used interchangeably. Another form of E2 is composed of amino acids 384 to 809 and a third form is associated with NS2. The non structural proteins are NS2, NS3, NS4 and NS5, of which at least NS4 and NS5 have been shown to be further processed into NS4A, NS4B, NS5A, and NS5B. **[0004]** Structural analysis of HCV genomes revealed the existence of different genotypes that have been classified into types and subtypes (Stuyver et al., 1993). The sequence diversities are distributed along the whole genome including the 5' untranslated region. The highest sequence variability has been observed in the NS2 and 3' untranslated regions, and in the putative envelope regions encoding the E1 and E2 proteins. The core, NS3, and certain regions of the NS4 proteins displayed markedly less diversity (Okamoto et al., 1992).

HCV humoral response

**[0005]** Soon after the discovery of HCV, immunoassays for the detection of circulating antibodies against HCV proteins became widely available. These tools have led to an explosive increase of the knowledge in the field of the human humoral immune response to HCV in different conditions. Once it was demonstrated that HCV was the major cause of posttransfusional non-A, non-B hepatitis, the search for antibodies to HCV was added to the safety screening panel of blood products. This procedure not only increased the safety of blood transfusions but also enhanced the knowledge of the epidemiology of the virus. The fact that HCV is responsible for a large proportion of chronic hepatic infections in which blood transfusion or parenteral inoculation are excluded remains a major challenge for further epidemiological studies. The widespread use of the assays for the detection of antibodies to HCV has also led to the recognition of the regions with humoral antigenicity of the virus. The relationship between the kinetics and magnitude of the humoral immune response to the different proteins of HCV and the course and outcome of the disease remains to be established.

HCV T cell epitopes

**[0006]** The immune response to viral antigens is almost entirely T cell dependent. T cells are required both for antibody production and for some cytotoxic reactions. HCV-encoded proteins are immunogenic not only at the B cell level, but also at the T cell level.

**[0007]** Studies describing the cellular immune response to HCV are scarce. Lin et al. (1993) describe candidate T cell epitopes within absolutely conserved regions of HCV gene obtained by means of a computer search revealing a large number of potential T cell epitopes. It has also been reported that peripheral blood cell monocytes (PBMC) from HCV-infected individuals proliferate in response to HCV recombinant proteins and that peripheral responses to core protein correlate with a benign course of infection (Botarelli et al., 1993). In the liver of patients with chronic HCV infection HCV-specific, HLA class I-restricted cytotoxic T lymphocytes (CTL) have been identified and cloned that recognize epitopes in E1 and NS2 proteins. These investigators have mainly focused on obtaining T cell clones from individual patients, and on the localization of the immunoreactive domain for the single CTL clones. Such studies led to the discovery of the epitope ASRCWVAM (aa 235-242) in the aminoterminal part of the E1 protein, and of the epitope LMALTSPYYKRY (aa 826-838) from the NS2 region (Koziel et al., 1992). In patients with chronic HCV hepatitis intrahepatic CD4<sup>+</sup> T cells which specifically recognized the NS4 protein of HCV were observed. The clonotype of these

T lymphocytes was not detectable in the PBMC from these subjects (Minutello et al., 1993). These studies demonstrate that in patients with HCV hepatitis, HCV-specific T lymphocytes can be isolated from the infected liver and the peripheral blood. Their role in the pathogenesis of the liver damage in HCV hepatitis and their relevance for the clearance or persistence of the virus remains to be established.

**[0008]** Although neutralization of certain viral infections is possible by humoral immunity only, most microbiological agents can only be cleared from the host with the aid of cellular immunity. Even when the neutralizing capacity of circulating antibodies is established in certain infections, T helper cell activity is generally required to allow B cells to produce the required levels of circulating antibodies, for achievement of neutralization and clearance of the infectious agent. However, certain infectious agents can only be neutralized by means of cellular immunity.

**[0009]** In the case of hepatitis C virus, it can be anticipated that T cell immunity may be required for clearance of the virus, since most patients enter into a chronic course of the disease, and since most patients infected with HCV have developed humoral immunity to most of the HCV antigens which can be employed for diagnosis of HCV infection, as described in patent applications no. EP-A-0 318 216, EP-A-0 388 232, EP-A-0 442 394, EP-A-0 484 787, EP-A-0 489 968. However, most of the antibody-positive patients have not been able to clear the virus from the circulation since they remain HCV-PCR positive and, consequently, the detected antibodies have not been protective neither sufficient to neutralize the virus. Possibly, antibodies to other epitopes which are currently not included in HCV diagnostic assays may be capable of neutralizing HCV infection. Such epitopes may be located on the viral membrane proteins E1 and E2, but protection against a wide range of different HCV species may be hampered by the hypervariability of HCV envelope regions.

**[0010]** The aim of the present invention is to provide T cell stimulating polypeptides and peptides derived from the HCV structural region.

**[0011]** Another aim of the present invention is to provide T cell stimulating polypeptides and peptides as defined above for use in the preparation of an HCV immunogenic composition.

**[0012]** Another aim of the present invention is to provide T cell stimulating peptides or polypeptides derived from the core region, of HCV.

**[0013]** Another aim of the present invention is to provide T cell stimulating peptides or polypeptides from HCV as specified above which contain either T helper cell (CD4<sup>+</sup>) epitopes and/or CTL (CD8<sup>+</sup>) epitopes.

**[0014]** Another aim of the present invention is to provide recombinant polypeptides containing the same.

**[0015]** Another aim of the present invention is to provide therapeutic as well as prophylactic compositions comprising the same.

**[0016]** Another aim of the present invention is to provide prophylactic or therapeutic compositions comprising said polypeptides.

**[0017]** Another aim of the present invention is to provide methods for preventing or treating HCV infection based on the same.

#### Detailed description of the invention

**[0018]** More particularly, the present invention describes a polypeptide of about 8 to about 20 amino acids comprising or consisting of at least 8 contiguous amino acids selected from the core region of the HCV polyprotein, with said contiguous amino acids containing a T-cell stimulating epitope, and provided that said polypeptide is different from any known T cell epitope containing HCV peptide or polypeptide described from any of the above-mentioned regions. The latter known HCV polypeptides and peptides are described for screening for B cell epitopes. Such polypeptides and peptides are for instance mentioned in EP-A-0 318 216, EP-A-0 388 232, EP-A-0 442 394, EP-A-0 484 787, EP-A-0 489 968, WO 92/22571, Lesniewski et al., 1993; Weiner et al., 1993; etc. The content of these applications is hereby incorporated by reference.

**[0019]** Even more particularly, the present invention relates to the use of polypeptides as described above for the preparation of an HCV immunogenic composition.

**[0020]** The expression "HCV immunogenic composition" refers to the prevention or treatment of HCV infection.

**[0021]** Preferentially said polypeptide is different from RALAHGVRVLEDG.

**[0022]** The term "HCV polyprotein" refers to any HCV polyprotein disclosed in the art and is reviewed in Okamoto et al. 1992, such as the type 1a HCV polyprotein of the HC-J1 isolate, such as the HCV polyprotein of the type 2a HC-J6 isolate (Okamoto et al., 1991), the type 2b HC-J8 isolate (Okamoto et al., 1992). According to this definition, any variation already observed within any of the described regions of HCV is to be considered as part of the definition of HCV polyprotein. For example, numerous types and subtypes are disclosed in Bukh et al., 1993, Bukh et al., 1994, Stuyver et al., 1993a, Stuyver et al., 1993b, Stuyver et al., 1994a, Stuyver et al., 1994c. Moreover, conservative substitutions may be introduced in these HCV polyproteins according to the present invention. The term "conservative substitution" as used herein denotes that one amino acid residue has been replaced by another, biologically similar residue. Examples of conservative substitutions include the substitution of one hydrophobic residue such as isoleucine,

valine, leucine or methionine for another, or the substitution of one polar residue for another such as between arginine and lysine, between glutamic and aspartic acids or between glutamine and asparagine and the like. The term "conservative substitution" also includes the use of a substituted amino acid in place of an unsubstituted parent amino acid provided that antibodies raised to such a polypeptide also immunoreact with the corresponding polypeptide having the unsubstituted amino acid.

**[0023]** The term "antibody" refers to a molecule that is a member of a family of glycosylated proteins called immunoglobulins, which can specifically combine with an antigen.

**[0024]** The word "antigen" has been used historically to designate an entity that is bound by an antibody, and also to designate the entity that induces the production of the antibody. More current usage limits the meaning of antigen to that entity bound by an antibody, while the word "immunogen" is used for the entity that induces antibody production. Where an entity discussed herein is both immunogenic and antigenic, reference to it as either an immunogen or antigen will typically be made according to its intended utility.

**[0025]** The term "corresponds" in its various grammatical forms as used in relation to peptide sequences means the peptide described plus or minus up to three amino acid residues at either or both of the amino- and carboxy-termini and containing only conservative substitutions in particular amino acid residues along the polypeptide sequence.

**[0026]** "Epitope" refers to that portion of a molecule that is specifically bound by a T cell antigen receptor or an antibody combining site.

**[0027]** The term "immunoreact" in its various forms means binding between an antigen as a ligand and a molecule containing an antibody combining site such as a Fab portion of a whole antibody.

**[0028]** The expression "T-cell stimulating epitope" or T cell epitope according to the present invention refers to an epitope capable of stimulating T-cells. A T-cell stimulating epitope may be selected according to the present invention by monitoring the lymphoproliferative response (as detailed in the Examples section) towards polypeptides containing in their amino acid sequence at least 8 contiguous amino acids derived from the core region of any HCV polyprotein. Said lymphoproliferative response may be measured by either a T-helper assay comprising in vitro stimulation of PMBC from patients with hepatitis C infection with varying concentrations of peptides to be tested for T-cell stimulating activity and counting the amount of radiolabelled thymidine uptake. Said lymphoproliferative response may also be measured by means of a CTL assay measuring the lytic activity of cytotoxic cells using  $^{51}\text{Cr}$  release. Proliferation is considered positive when the stimulation index (mean cpm of antigen-stimulated cultures/mean cpm of control cultures) is more than 1, preferably more than 2, most preferably more than 3. In order to select a T-cell stimulating epitope containing peptide, the results of these lymphoproliferative assays are compared and immunodominant T-cell epitope containing polypeptides or peptides are selected. The results of the lymphoproliferative assays against certain peptides may also be compared between clinical non-responders and responders to interferon- $\alpha$  treatment. The lymphoproliferative response towards a series of synthetic, overlapping peptides representing the HCV core, E1 and E2/NS1 sequences and a recombinant NS3 protein was monitored in 32 patients with chronic HCV hepatitis as disclosed in the Examples section of the present invention.

**[0029]** Consequently, the present invention represents a selection of immunodominant T cell epitopes from a series of antigens covering the core region. From the examples section, it is clear that not only peptide pools 2 and 3 and peptides NS1-5\* and NS1-7\* but also, pools 4, 5, 6 and 9 and NS3, reacted frequently with hepatitis C patients (Table 4) while infrequent reactivity could only be observed in normal controls with the same polypeptides (Table 5). It is obvious from the data presented in Table 4 that large areas of the HCV structural region, such as pool 1 (amino acids 5-72) and pools 7 and 8 (amino acids 427-578) show little reactivity with T cells of infected patients, even with patients with a response to IFN- $\alpha$  treatment. Most strikingly, however, it was found that while the dominant B cell response to hepatitis C in general is located to the core aminoterminal (see also Table 3), the dominant T cell response is directed towards the core carboxyterminal region (see Table 4). In the literature, ample evidence can be found that the core carboxyterminal half contains little or no B cell-reactive epitopes. Based on the present invention, it may be desirable to yet include for instance parts of the core carboxyterminal region (spanning amino acids 73-176) into prophylactic or therapeutic vaccine compositions.

**[0030]** The words "polypeptide" and "peptide" are used interchangeably throughout the specification and designate a linear series of amino acids connected one to the other by peptide bonds between the alpha-amino and carboxy groups of adjacent amino acids. Polypeptides can be a variety of lengths, either in their natural (uncharged) forms or in forms which are salts, and either free of modifications such as glycosylation, side chain oxidation, or phosphorylation or containing these modifications. It is well understood in the art that amino acid sequences contain acidic and basic groups, and that the particular ionization state exhibited by the peptide is dependent on the pH of the surrounding medium when the protein is in solution, or that of the medium from which it was obtained if the protein is in solid form. Also included in the definition are proteins modified by additional substituents attached to the amino acids side chains, such as glycosyl units, lipids, or inorganic ions such as phosphates, as well as modifications relating to chemical conversions of the chains, such as oxidation of sulfhydryl groups. Thus, "polypeptide" or its equivalent terms is intended to include the appropriate amino acid sequence referenced, subject to those of the foregoing modifications which do

not destroy its functionality.

**[0031]** The polypeptides of the invention, and particularly the shorter peptides amongst them, can be prepared by classical chemical synthesis. The synthesis can be carried out in homogeneous solution or in solid phase.

**[0032]** For instance, the synthesis technique in homogeneous solution which can be used is the one described by Houbenweyl in the book entitled "Methode der organischen chemie" (Method of organic chemistry) edited by B. Wunsh, vol. 15-I et II. THIEME, Stuttgart 1974.

**[0033]** The polypeptides of the invention can also be prepared in solid phase according to the methods described by Atherton and Shepard in their book entitled "Solid phase peptide synthesis" (IRL Press, Oxford, 1989).

**[0034]** The polypeptides according to this invention can also be prepared by means of recombinant DNA techniques as documented below.

**[0035]** The polypeptides or peptides according to the present invention may, as specified above, vary in length. The peptides according to the invention contain at least 8 contiguous HCV amino acids. Preferred lengths of peptides are 8, 9, 10, or more (for instance 15, 20, etc.) amino acid residues.

**[0036]** The expression "comprised between amino acids X to Y" includes the amino acid X and the amino acid Y.

**[0037]** The numbering of the HCV polyprotein used in the present invention refers to the numbering as used for the HCV-J isolate according to Kato et al., 1990. All other HCV isolates known in the art may be aligned to this sequence to obtain the referred HCV polyprotein numbering for each individual HCV isolate. For instance, it is known that type 2 isolates can contain 4 extra codons/amino acids in their E2 sequence, while type 3 sequences have an insertion of 2 amino acids compared to type 1 sequences.

**[0038]** The Examples section of the present invention describes T cell epitopes in, amongst other regions of the HCV structural region: the carboxyterminal region of the core protein (aa 73-176), amino acids 192 to 383 of the E1 region, amino acids 397 and 428 and amino acids 571 to 638 of the E2 region, amino acids 1188 to 1463 of the NS3 region. Groups of peptides covering parts of the structural proteins core and E2, and covering the complete E1 protein, as well as a recombinant NS3 protein have been studied. Peptides were tested as group 1 (aa 5-80), group 2 (aa 73-140), group 3 (aa 133-200), group 4 (aa 193-260), group 5 (aa 253-332), group 6 (325-392), group 7 (aa 427-494), group 8 (aa 487-578), and group 9 (aa 571-638) as shown in Table 1. Recombinant NS3 encompassed amino acids 1188 to 1463 of the isolate IG8309, belonging to the 1b subtype group of HCV.

**[0039]** The T cell response to the group 3 peptides, as well as to the individual peptides NS1-7\* and MS1-5\* shows a statistically relevant correlation with a decrease in alanine aminotransferase (ALT) and viral RNA levels, which are generally accepted to indicate a more benign course of the disease. A correlation between response to 'a recombinant HCV core protein' and a more benign course of the disease has been described by Botarelli et al. 1993. However, no epitopes have been mapped nor has the sequence and exact position of the recombinant core protein been described in Botarelli et al., 1993. In the present invention, a similar T cell response has been observed to the group 2 peptides (aa 73-140) both in patients responding to IFN- $\alpha$  and in patients non-responding to the same. On the contrary, T cell reactivity to the group 3 peptides (aa 133-200) was observed in responders to interferon- $\alpha$  and differed from the T cell reactivity observed to this region in non-responders to IFN- $\alpha$  treatment. Furthermore, after investigating the reactivity of individual peptides from groups 2 and 3, this specific response correlating with a more benign course of HCV infection, could be further mapped to specific individual peptides termed CORE 23, CORE 25, and CORE 27. Peptide CORE 19, belonging to the group 2 peptides, was also recognized by some of the responders to IFN- $\alpha$  treatment (see Fig. 1).

**[0040]** Preferentially said polypeptide of the present invention is different from RALAHGVRVLEDG spanning positions 149 to 161 of the core region of HCV.

**[0041]** The present invention relates to the use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 157 to 176 of the core region of HCV: NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGNX<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 51), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 13, and wherein X<sub>30</sub> represents V or A or L, X<sub>31</sub> represents L or V or I, X<sub>32</sub> represents E or G, X<sub>33</sub> represents V or I, and X<sub>34</sub> represents F or Y, X<sub>35</sub> represents A or P, X<sub>36</sub> represents L or I.

**[0042]** The present invention also relates to the use as described above, for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 157 to 176 of the core region of HCV: VLEDGVNYATGN-LPGCSFSI (SEQ ID NO 13 = peptide CORE 27) or VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73).

**[0043]** The present invention also relates to the use, as described above, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

$\text{NH}_2\text{-GX}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 74),  
 $\text{NH}_2\text{-X}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 75),  
 $\text{NH}_2\text{-NX}_{38}\text{PGCSFSI-COOH}$  (SEQ ID NO 76) and  
 $\text{NH}_2\text{-X}_{38}\text{PGCSFSI-COOH}$  (SEQ ID NO 77).

[0044] The present invention also relates to the use as described above, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

$\text{GVNYATGNL}$  (SEQ ID NO 78),  
 $\text{NLPGCSFSI}$  (SEQ ID NO 80) and  
 $\text{LPGCSFSI}$  (SEQ ID NO 81).

[0045] The present invention also relates to the use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 145 to 164 of the core region of HCV:

$\text{NH}_2\text{-GGX}_{25}\text{X}_{26}\text{X}_{27}\text{X}_{28}\text{LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 52), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 12, and wherein  $\text{X}_{25}$  represents A or V,  $\text{X}_{26}$  represents A or S,  $\text{X}_{27}$  represents R or A,  $\text{X}_{28}$  represents A or T or E,  $\text{X}_{29}$  represents A or E,  $\text{X}_{30}$  represents V or A or L,  $\text{X}_{31}$  represents L or V or I,  $\text{X}_{32}$  represents E or G,  $\text{X}_{33}$  represents V or I, and  $\text{X}_{34}$  represents F or Y.

[0046] The present invention also relates to the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 145 to 164 of the core region of HCV:

$\text{GGAARALAHGVRVLEDGVNY}$  (SEQ ID NO 12 = peptide CORE 25) or  
 $\text{GGVAARALAHGVRVLEDGVNY}$  (SEQ ID NO 118).

[0047] The present invention also contemplates the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

$\text{NH}_2\text{-X}_{28}\text{LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{-COOH}$  (SEQ ID NO 82),  $\text{NH}_2\text{-LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{-COOH}$  (SEQ ID NO 83),  $\text{NH}_2\text{-GVRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{-COOH}$  (SEQ ID NO 84),  $\text{NH}_2\text{-VRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{-COOH}$  (SEQ ID NO 85),  $\text{NH}_2\text{-RX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 86), and  $\text{NH}_2\text{-X}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 87).

[0048] The present invention also relates to the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:  $\text{ALAHGVRVL}$  (SEQ ID NO 88),  $\text{LAHGVRVL}$  (SEQ ID NO 89),  $\text{VRVLEDGV}$  (SEQ ID NO 90),  $\text{RVLEDGV}$  (SEQ ID NO 91),  $\text{VLEDGVNY}$  (SEQ ID NO 92), and  $\text{LEDGVNY}$  (SEQ ID NO 93).

[0049] The present invention also relates to the use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 133 to 152 or the core region of HCV:

$\text{NH}_2\text{-LX}_{19}\text{X}_{20}\text{YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{X}_{26}\text{X}_{27}\text{X}_{28}\text{LX}_{29}\text{-COOH}$  (SEQ ID NO 53), and with said contiguous amino

acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 11, and wherein  $X_{19}$  represents M or I,  $X_{20}$  represents G or E,  $X_{21}$  represents L or V or I,  $X_{22}$  represents V or L,  $X_{23}$  represents A or G,  $X_{24}$  represents L, V or I,  $X_{25}$  represents A or V,  $X_{26}$  represents A or S,  $X_{27}$  represents R or A,  $X_{28}$  represents A or T or E,  $X_{29}$  represents A or E.

**[0050]** The present invention also relates the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 133 to 152 of the core region of HCV:

**LMGYIPLVGAPLGGAARALA (SEQ ID NO 11 = peptide CORE 23) .**

**[0051]** The present invention also relates the use as described above for the preparation of an HCV Immunogenic composition, with said polypeptide being chosen from the following list of peptides:

**$NH_2-X_{19}X_{20}YIPX_{21}X_{22}GX_{23}PX_{24}GGX_{25}-COOH$  (SEQ ID NO 62),**

**$NH_2-X_{19}X_{20}YIPX_{21}X_{22}GX_{23}PX_{24}GGX_{25}-COOH$  (SEQ ID NO 63),**

**$NH_2-YIPX_{21}X_{22}GX_{23}PX_{24}-COOH$  (SEQ ID NO 64),**

**$NH_2-IPX_{21}X_{22}GX_{23}PX_{24}-COOH$  (SEQ ID NO 65),**

**$NH_2-X_{21}X_{22}GX_{23}PX_{24}GGX_{25}-COOH$  (SEQ ID NO 66), and**

**$NH_2-X_{22}GX_{23}PX_{24}GGX_{25}-COOH$  (SEQ ID NO 68)**

The present invention also relates to the use as described above for the preparation of an HCV Immunogenic composition, with said polypeptide being chosen from the following list of peptides:

**LMGYIPLV (SEQ ID NO 69), MGYIPLV (SEQ ID NO 70), YIPLVGAPL (SEQ ID NO 71),  
IPLVGAPL (SEQ ID NO 72), LVGAPLGGA (SEQ ID NO 94), and VGAPLGGA (SEQ ID NO 95).**

**[0052]** The present invention also relates to the use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 109 to 128 of the core region of HCV:

**$NH_2-X_{11}X_{12}DPRX_{13}X_{14}SRNX_{15}GX_{16}VIDTX_{17}TC-COOH$  (SEQ ID NO 54), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 9, and wherein  $X_{11}$  represents P or Q,  $X_{12}$  represents N or T,  $X_{13}$  represents R or H,  $X_{14}$  represents R or K,  $X_{15}$  represents L or V or F,  $X_{16}$  represents K or R,  $X_{17}$  represents L or I.**

**[0053]** The present invention also relates to the use as described above for the preparation of an HCV Immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 109 to 128 of the core region of HCV: **PTDPRRRSRNLG-KVIDTLTC (SEQ ID NO 9 = peptide CORE 19).**

**[0054]** The present invention also relates to the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following peptides:  **$NH_2-NX_{15}GX_{16}VIDTX_{17}-COOH$  (SEQ ID NO 96), and  $NH_2-X_{15}GX_{16}VIDTX_{17}-COOH$  (SEQ ID NO 97).**

**[0055]** The present invention also relates to the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following peptides:

**NLGKVIDTL (SEQ ID NO 98), and LGKVIDTL (SEQ ID NO 117).**

**[0056]** The present invention also relates to the use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of at least 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 73 to 92 of the core

region of HCV:

NH<sub>2</sub>-GX<sub>1</sub>X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PWPLYX<sub>6</sub>NX<sub>7</sub>GX<sub>8</sub>G-COOH (SEQ ID NO 99), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 6, and wherein X<sub>1</sub> represents R or K, X<sub>2</sub> represents A, S or T, X<sub>3</sub> represents A or G, X<sub>4</sub> represents Q, K or R, X<sub>5</sub> represents Y or H, X<sub>6</sub> represents G or A, X<sub>7</sub> represents E or K, and X<sub>8</sub> represents C, M or L.

[0057] The present invention also relates to the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of a least 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 73 to 92 of the core region of HCV:

**GRTWAQPGYPWPLYGNEGCG (SEQ ID NO 6 = peptide CORE 13).**

[0058] The present invention also relates to the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide being selected from:

**NH<sub>2</sub>-X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 100) and NH<sub>2</sub>-WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 101).**

[0059] The present invention also relates to the use as described above for the preparation of an HCV immunogenic composition, with said polypeptide being selected from:

**TWAQPGYPW (SEQ ID NO 102), and WAQPGYPW (SEQ ID NO 103).**

[0060] The present invention relates more particularly to any of the above-mentioned uses wherein said T cell stimulating epitope is a T cell helper epitope.

[0061] According to another embodiment, the present invention relates to any of the above-mentioned uses wherein said T cell stimulating epitope is a CTL epitope.

[0062] The present invention also relates to any of the above-mentioned uses, wherein said polypeptide is incorporated into a prophylactic vaccine composition.

[0063] According to another embodiment, the present invention relates to any of the above-mentioned uses, wherein said polypeptide is incorporated into a therapeutic vaccine composition.

[0064] Moreover, the present invention also contemplates a polypeptide consisting of multiple repeats, combinations or mimotopes of any of the contiguous amino acid sequences selected to contain a T-cell stimulating epitopes as defined above, with said combinations comprising two or more peptides joined into a single structure and with said mimotopes having one or more amino acid variations compared to said peptides as long as said mimotope peptides are capable of providing for immunological stimulation after which the T-cells are reactive with at least one strain of HCV.

[0065] The term "mimotopes" refers to peptides which mimic the polypeptides as defined above immunologically. Since sequence variability has been observed from HCV, it may be desirable to vary one or more amino acids so as to better mimic the epitopes of different strains. It should be understood that such mimotopes need not be identical to any particular HCV sequence as long as the subject compounds are capable of providing for immunological stimulation after which the T cells are reactive with at least one strain of HCV. The polypeptides as described above, may therefore be subject to insertions, deletions and conservative as well as non-conservative amino acid substitutions where such changes might provide for certain advantages in their use. The peptides will preferably be as short as possible while still maintaining all of their sensitivity of the larger sequence. In certain cases, it may be desirable to join two or more peptides into a single structure. The formation of such a composite may involve covalent or non-covalent linkages.

[0066] The present invention also contemplates the uses as defined above, with said polypeptide being a recombinant polypeptide expressed by means of an expression vector comprising a nucleic acid insert encoding a polypeptide as defined above.

[0067] The present invention relates also to the use of a recombinant expression vector comprising a nucleic insert encoding a polypeptide as defined herein, for the preparation of a HCV immunogenic composition. In order to carry out the expression of the T-cell containing polypeptides of the invention in bacteria such as E. coli or in eukaryotic cells such as in S. cerevisiae, or in cultured vertebrate or invertebrate hosts such as insect cells, Chinese Hamster Ovary



(CHO), COS1, BHK, and MDCK cells, the following steps are carried out:

- transformation of an appropriate cellular host with a recombinant vector, or by means of adenoviruses, influenza viruses, BCG, and any other live carrier systems, in which a nucleotide sequence coding for one of the polypeptides of the invention has been inserted under the control of the appropriate regulatory elements, particularly a promoter recognized by the polymerases of the cellular host or of the live carrier system and in the case of a prokaryotic host, an appropriate ribosome binding site (RBS), enabling the expression in said cellular host of said nucleotide sequence,
- culture of said transformed cellular host under conditions enabling the expression of said insert. Recombinant virus or live carrier vectors may also be directly used as live vaccines in humans.

**[0068]** According to a preferred embodiment, the present invention contemplates any of the uses as defined above wherein said polypeptide is operably linked to a pathogen related immunogen such as the HCV envelope proteins E1 and E2, or the HCV NS3, NS4 or NS5 immunogens, or a HCV peptide containing a B cell epitope.

**[0069]** The phrase "operatively linked" as used herein means that the linkage does not interfere with the ability of either of the linked groups to function as described, e.g., to function as a T or B cell determinant. Thus, operatively linking not only includes covalent linkages, but also includes linkages capable of inducing T cell function.

**[0070]** The phrase "pathogen related" as used herein designates a polypeptide that is capable of inducing the T cell function that immunoreacts with a pathogen in native form.

**[0071]** The defined polypeptides can be employed as such or in combination with HCV B cell epitopes, HBsAg or HBcAg particles, HBV immunogens, HIV immunogens, HTLV immunogens HCV peptides containing preferred B cell epitopes are detailed in for instance EP-A-0 489 968 and WO 93/18054.

**[0072]** Methods for operatively linking individual polypeptides through an amino acid residue side chain to form an immunogenic conjugate, i.e., a branched-chain polypeptide polymer, are well known in the art. Those methods include linking through one or more types of functional groups on various side chains and result in the respective polypeptide backbones being covalently linked (coupled) but separated by at least one side chain.

**[0073]** Useful side chain functional groups include epsilon-amino groups, beta- or gamma-carboxyl groups, thiol (-SH) groups and aromatic rings (e.g. tyrosine and histidine). Methods for linking polypeptides using each of the above functional groups are described in Erlanger (1980), Aurameas et al. (1978) and U.S. Patent No. 4,493,795 to Nestor et al.. In addition, a site-directed coupling reaction; as described in Rodwell et al. (1985), can be carried out so that the biological activity of the polypeptides is not substantially diminished.

**[0074]** Furthermore, as is well known in the art, the HBcAg protein and polypeptide immunogen can be used in their native form or their functional group content may be modified by succinylation of lysine residues or reaction with cysteine-thiolactone. A sulfhydryl group may also be incorporated into either polypeptide by reaction of amino functions with 2-iminothiolane or the N-hydroxysuccinimide ester of 3-(3-dithiopyridyl) propionate. The polypeptides can also be modified to incorporate spacer arms, such as hexamethylene diamine or other bifunctional molecules of similar size, to facilitate linking.

**[0075]** Any polypeptide immunogen against which antibody production is desired can be linked to the polypeptide of the present invention protein to form an immunogenic conjugate of this invention. In preferred embodiments the polypeptide immunogen is a pathogen related immunogen and the conjugate has the capacity to induce the production of antibodies that immunoreact with the pathogen when injected in an effective amount into an animal. Exemplary immunogens of particular importance are derived from bacteria such as B. pertussis, S. typosa, S. Paratyphoid A and B. C. diptheriae, C. tetani, C. botulinum, C. perfringens, B. anthracis, P. pestis, P. multocida, V. cholerae, N. meningitides, N. gonorrhea, H. influenzae, T. palladium, and the like; immunogens derived from viruses such as polio virus, adenovirus, parainfluenza virus, measles, mumps, respiratory syncytical virus, influenza virus, equine encephalomyelitis virus, hog cholera virus, Newcastle virus, fowl pox virus, rabies virus, feline and canine distemper viruses, foot and mouth disease virus, human and simian immunodeficiency viruses, and the like; rickettsiae immunogen such as epidemic and endemic typhus, and the spotted fever groups, and the like. Immunogens are well known to the prior art in numerous references such as U.S. Patent No. 3,149,036, No. 3,983,228, and No. 4,069,313; in Essential Immunology, 3rd Ed., by Roit, published by Blackwell Scientific Publications; in Fundamentals of Clinical Immunology, by Alexander and Good, published by W.B. Saunders; and in Immunology, by Bellanti, published by W.B. Saunders. Particularly preferred pathogen related immunogens are those described in United States Patent No. 4,625,015, No. 4,544,500, No. 4,545,931, No. 4,663,436, No. 4,631,191, No. 4,629,783 and in Patent Cooperation Treaty International Publication No. WO87/02775 and No. WO87/02892 all of whose disclosures are incorporated herein by reference.

**[0076]** The present invention relates particularly to a peptide consisting of at least 8 contiguous amino acids of the sequence of any of the following peptides, with said peptides containing a T-cell epitope:

NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 51)

VLEDGVNYATGNLPGCSFSI (SEQ ID NO 13 = peptide CORE 27),

VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73),

NH<sub>2</sub>-GX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>-COOH (SEQ ID NO 74),

NH<sub>2</sub>-X<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>-COOH (SEQ ID NO 75),

NH<sub>2</sub>-NX<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 76),

NH<sub>2</sub>-X<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 77),

GVNYATGNL (SEQ ID NO 78),

NLPGCSFSI (SEQ ID NO 80), or LPGCSFSI (SEQ ID NO 81),

wherein said peptide mimics the T-cell immunological stimulation properties of the peptide represented in SEQ ID NO 13;

NH<sub>2</sub>-GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 52),

GGAARALAHGVRVLEDGVNY (SEQ ID NO 12 = peptide CORE 25),

GGVAARALAHGVRVLEDGVNY (SEQ ID NO 118),

NH<sub>2</sub>-X<sub>29</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 82),

NH<sub>2</sub>-LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 83),

NH<sub>2</sub>-GVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 84),

NH<sub>2</sub>-VRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 85),

NH<sub>2</sub>-RX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 86),

NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 87),

ALAHGVRVL (SEQ ID NO 88), LAHGVRVL (SEQ ID NO 89),

VRVLEDGV (SEQ ID NO 90), RVLEDGV (SEQ ID NO 91), VLEDGVNY (SEQ ID NO

92), or LEDGVNY (SEQ ID NO 93),

wherein said peptide mimics the T-cell immunological stimulation properties of the peptide represented in SEQ ID NO 12;

NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>-COOH (SEQ ID NO 53),

LMGYIPLVGAPLGGAARALA (SEQ ID NO 11 = peptide CORE 23),

NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 62),

NH<sub>2</sub>-X<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 63),

NH<sub>2</sub>-YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 64),

NH<sub>2</sub>-IPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 65),  
 NH<sub>2</sub>-X<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 66),  
 NH<sub>2</sub>-X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 68),  
 LMGYIPLV (SEQ ID NO 69), MGYIPLV (SEQ ID NO 70),  
 YIPLVGAPL (SEQ ID NO 71), IPLVGAPL (SEQ ID NO 72),  
 LVGAPLGGGA (SEQ ID NO 94), or VGAPLGGGA (SEQ ID NO 95),

wherein said peptide mimics the T-cell immunological stimulation properties of the peptide represented in SEQ ID NO 11;

NH<sub>2</sub>-X<sub>11</sub>X<sub>12</sub>DPRX<sub>13</sub>X<sub>14</sub>SRNX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>TC -COOH (SEQ ID NO 54),  
 PTDPRRRSRNLGKVIDTLTC (SEQ ID NO 9 = peptide CORE 19),  
 NH<sub>2</sub>-NX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 96),  
 NH<sub>2</sub>-X<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 97),  
 NLGKVIDTL (SEQ ID NO 98), or LGKVIDTL (SEQ ID NO 117),

wherein said peptide mimics the T-cell Immunological stimulation properties of the peptide as represented in SEQ ID NO 9;

NH<sub>2</sub>-GX<sub>1</sub>X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PWPLYX<sub>6</sub>NX<sub>7</sub>GX<sub>8</sub>G-COOH (SEQ ID NO 99),  
 GRTWAQPGYPWPLYGNEGCG (SEQ ID NO 6 = peptide CORE 13),  
 NH<sub>2</sub>-X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 100),  
 NH<sub>2</sub>-WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 101),  
 TWAQPGYPW (SEQ ID NO 102), or WAQPGYPW (SEQ ID NO 103),

wherein said peptida mimics the T-cell immunological stimulation properties of the peptide as represented in SEQ ID NO 6;

wherein X<sub>1</sub> represents R or K, X<sub>2</sub> represents A, S or T, X<sub>3</sub> represents A or G, X<sub>4</sub> represents Q, K or R, X<sub>5</sub> represents Y or H, X<sub>6</sub> represents G or A, X<sub>7</sub> represents E or K, X<sub>8</sub> represents C, M or L, X<sub>9</sub> represents W or L, X<sub>10</sub> represents S, N, T, D or H, X<sub>11</sub> represents P or Q, X<sub>12</sub> represents N or T, X<sub>13</sub> represents R or H, X<sub>14</sub> represents R or K, X<sub>15</sub> represents L or V or F, X<sub>16</sub> represents K or R, X<sub>17</sub> represents L or I, X<sub>18</sub> represents F or L, X<sub>19</sub> represents M or I, X<sub>20</sub> represents G or E, X<sub>21</sub> represents L or V or I, X<sub>22</sub> represents V or L, X<sub>23</sub> represents A or G, X<sub>24</sub> represents L, V or I, X<sub>25</sub> represents A or V, X<sub>26</sub> represents A or S, X<sub>27</sub> represents R or A, X<sub>28</sub> represents A or T or E, X<sub>29</sub> represents A or E, X<sub>30</sub> represents V or A or L, X<sub>31</sub> represents L or V or I, X<sub>32</sub> represents E or G, X<sub>33</sub> represents V or I, X<sub>34</sub> represents F or Y, X<sub>35</sub> represents A or P, and X<sub>36</sub> represents L or I.

**[0077]** Moreover, the present invention contemplates an imminogenic composition consisting of or comprising at least one of the polypeptides as defined above mixed with a pharmaceutically acceptable excipient.

**[0078]** Before administration to patients, formulants may be added to the polypeptides or peptides of the invention. A liquid formulation is preferred. For example, these formulants may include oils, polymers, vitamins, carbohydrates, amino acids, salts, buffers, albumin, surfactants, or bulking agents. Preferably carbohydrates include sugar or sugar alcohols such as mono, di, or polysaccharides, or water soluble glucans. The saccharides or glucans can include fructose, dextrose, lactose, glucose, mannose, sorbose, xylose, maltose, sucrose, dextran, pullulan, dextrin, alpha and beta cyclodextrin, soluble starch, hydroxethyl starch and carboxymethylcellulose, or mixtures thereof. Sucrose is most preferred. "Sugar alcohol" is defined as a C4 to C8 hydrocarbon having an -OH group and includes galactitol, inositol, mannitol, xylitol, sorbitol, glycerol, and arabitol. Mannitol is most preferred. These sugars or sugar alcohols mentioned above may be used individually or in combination. There is no fixed limit to amount used as long as the

sugar or sugar alcohol is soluble in the aqueous preparation. Preferably, the sugar or sugar alcohol concentration is between 1.0 w/v% and 7.0 w/v%, more preferable between 2.0 and 6.0 w/v%. Preferably amino acids include levorotary (L) forms of carnitine, arginine, and betaine; however, other amino acids may be added. Preferred polymers include polyvinylpyrrolidone (PVP) with an average molecular weight between 2,000 and 3,000, or polyethylene glycol (PEG) with an average molecular weight between 3,000 and 5,000. It is also preferred to use a buffer in the composition to minimize pH changes in the solution before lyophilization or after reconstitution. Most any physiological buffer may be used, but citrate, phosphate, succinate, and glutamate buffers or mixtures thereof are preferred. Most preferred is a citrate buffer. Preferably, the concentration is from 0.01 to 0.3 molar. Surfactants that can be added to the formulation are shown in EP patent applications No. EP 0 270.799 and EP 0 268 110.

**[0079]** Additionally, polypeptides can be chemically modified by covalent conjugation to a polymer to increase their circulating half-life, for example. Preferred polymers, and methods to attach them to peptides, are shown in U.S. Patent Nos. 4,766,106; 4,179,337; 4,495,285; and 4,609,546. Preferred polymers are polyoxyethylated polyols and polyethylene glycol (PEG). PEG is soluble in water at room temperature and has the general formula:  $R(O-CH_2-CH_2)_nO-R$  where R can be hydrogen, or a protective group such as an alkyl or alkanol group. Preferably, the protective group has between 1 and 8 carbons, more preferably it is methyl. The symbol n is a positive integer, preferably between 1 and 1,000, more preferably between 2 and 500. The PEG has a preferred average molecular weight between 1000 and 40,000, more preferably between 2000 and 20,000, most preferably between 3,000 and 12,000. Preferably, PEG has at least one hydroxy group, more preferably it is a terminal hydroxy group. It is this hydroxy group which is preferably activated. However, it will be understood that the type and amount of the reactive groups may be varied to achieve a covalently conjugated PEG/polypeptide of the present invention.

**[0080]** Water soluble polyoxyethylated polyols are also useful in the present invention. They include polyoxyethylated sorbitol, polyoxyethylated glucose, polyoxyethylated glycerol (POG), etc. POG is preferred. One reason is because the glycerol backbone of polyoxyethylated glycerol is the same backbone occurring naturally in, for example, animals and humans in mono-, di-, triglycerides. Therefore, this branching would not necessarily be seen as a foreign agent in the body. The POG has a preferred molecular weight in the same range as PEG. The structure for POG is shown in Knauf et al., 1988, and a discussion of POG/L-2 conjugates is found in U.S. Patent No. 4,766,106.

**[0081]** Another drug delivery system for increasing circulatory half-life is the liposome. Methods of preparing liposome delivery systems are discussed in Gabizon et al., 1982; and Szoka, 1980. Other drug delivery systems are known in the art and are described in, e.g. Poznansky, 1984.

**[0082]** After the liquid pharmaceutical composition is prepared, it is preferably lyophilized to prevent degradation and to preserve sterility. Methods for lyophilizing liquid compositions are known to those of ordinary skill in the art. Just prior to use, the composition may be reconstituted with a sterile diluent (Ringer's solution, distilled water, or sterile saline, for example) which may include additional ingredients. Upon reconstitution, the composition is preferably administered to subjects using those methods that are known to those skilled in the art.

**[0083]** As stated above, the polypeptides and compositions of this invention are used to treat human patients to prevent or treat any of the above-defined disease states. The preferred route of administration is parenterally. In parenteral administration, the compositions of this invention will be formulated in a unit dosage injectable form such as a solution, suspension or emulsion, in association with a pharmaceutically acceptable parenteral vehicle. Such vehicles are inherently nontoxic and nontherapeutic. Examples of such vehicles are saline, Ringer's solution, dextrose solution, and Hanks' solution. Nonaqueous vehicles such as fixed oils and ethyl oleate may also be used. A preferred vehicle is 5% dextrose in saline. The vehicle may contain minor amounts of additives such as substances that enhance isotonicity and chemical stability, including buffers and preservatives.

**[0084]** The dosage and mode of administration will depend on the individual.

**[0085]** More particularly, the present invention contemplates a composition as defined above for use in a method of immunizing against HCV, comprising administering a sufficient amount of at least one of the polypeptides as defined above, possibly accompanied by pharmaceutically acceptable adjuvants, to produce an immune response.

**[0086]** More particularly, said immunogenic composition is a vaccine composition. Even more particularly, said vaccine composition is a prophylactic vaccine composition. Alternatively, said vaccine composition may also be a therapeutic vaccine composition.

**[0087]** The prophylactic vaccine composition refers to a vaccine composition aimed for preventing HCV infection and to be administered to normal persons who are not yet infected with HCV.

**[0088]** The therapeutic vaccine composition refers to a vaccine composition aimed for treatment of HCV infection and to be administered to patients being infected with HCV.

**[0089]** The polypeptides described in the present invention can be modified with lipid (lipopeptides, e.g.  $PAM_3Cys$ ), and formulated with alum, monophosphoryl lipid A, pluronics, SAF1, Ribl, trehalose-6,6-dimycolate or other immunostimulating compounds known to those skilled in the art, as to enhance their immunogenicity.

**[0090]** Also, the present invention contemplates according to a preferred embodiment, a composition as defined above, with said composition comprising in addition to any of the T cell-stimulating polypeptides as defined above, a

peptide or polypeptide containing at least one B-cell epitope of HCV, and/or a structural HCV polypeptide, and/or a non-structural HCV polypeptide.

[0091] According to a yet other preferred embodiment, the present invention contemplates a composition as defined above for use in a method of treatment of HCV, comprising administering a sufficient amount of at least one of the polypeptides as defined above, possibly accompanied by pharmaceutically acceptable adjuvants, to allow treatment of HCV infection. In this case the polypeptides of the present invention can be employed in the form of therapeutic vaccine, aiming at the induction of a sufficient level of T cell function for clearance of Hepatitis C virus infection.

[0092] According to yet another preferred embodiment, the present invention contemplates a composition as defined above, with said composition comprising in addition to any of the polypeptides as defined above, a peptide or polypeptide containing at least one B-cell epitope of HCV, and/or a structural HCV polypeptide, and/or a non-structural HCV polypeptide.

[0093] According to yet another embodiment, the present invention contemplates a composition wherein said polypeptides as defined above are mixed with HBsAg or HBcAg particles, HBV immunogens, HIV immunogens and/or HTLV immunogens.

#### **Figure legends**

[0094] **Figure 1:** Evolution of the lymphoproliferative responses and transaminase activities in HCV patient No. 632. AST depicts aspartate aminotransferase, ALT depicts alanine aminotransferase; SI: simulation index; P1 to P6 refers to the groups of peptides 1 to 6 as disclosed in Table 1.

[0095] **Figure 2:** Frequencies of lymphoproliferation responses to peptide pools 1-9, single peptides NS1-7\*, NS1-5\* and recombinant NS3 protein in healthy controls, interferon (IFN) responders and IFN non-responders.

[0096] **Figure 3:** represents the part of the sequence of the isolate IG8309 which has been tested, with said part extending from with Gly at position 41 to Ser at position 318 (SEQ ID NO 57).

[0097] **Figure 4:** represents an alignment of the HCV structural regions.

[0098] **Figure 5.** Alignment of E2 region spanning amino acid positions 571 to 638.

[0099] **Figure 6.** Alignment of NS3 sequences spanning amino acid positions 1188 to 1465.

#### **EXAMPLES**

##### **Example 1. Patients studied**

[0100] The patients studied consisted of 19 males and 13 females, aged between 27 and 71 (mean age: 49.9 years). The diagnosis of chronic HCV hepatitis was based on a) a documented elevation of alanine aminotransferase of 2 times the upper limit of normal for at least six months; b) the presence of HCV-specific serum antibodies detected by two second generation enzyme immunoassay tests (UBI test and Innostest HCV AbII, Innogenetics, Antwerp Belgium) and c) absence of clinical, histological or serological signs of other viral, toxic, metabolic, hereditary or auto-immune hepatitis. The patients were randomized to receive either the standard treatment consisting of 3 million units Interferon  $\alpha$ -2b (INTRON A) given thrice weekly for 24 weeks or an experimental treatment consisting of an induction phase of 6 million units Interferon  $\alpha$ -2b thrice weekly for eight weeks, followed by a maintenance phase of titrated doses of interferon of 6 to 1 million units thrice weekly until biochemical and virological remission (alanine aminotransferase activity normal, plasma hepatitis C virus-RNA undetectable) was achieved. Patients were considered clinical responders when a normalization of alanine aminotransferase activity was observed on at least two successive control visits during treatment with at least one month interval.

[0101] As controls for the specificity of the lymphoproliferative responses, 18 healthy individuals aged 25-58 years (mean 38.6), 10 males and 8 females were selected. These subjects were negative for HCV antibodies and HCV-RNA. One subject had a history of past hepatitis B virus infection and 7 had antibodies to HBsAg as a result of vaccination.

[0102] A liver biopsy was performed in all patients prior to the initiation of Interferon- $\alpha$  therapy. The histological status was defined according to conventional histological classification (Knodell et al., 1981).

[0103] Based on the definition of clinical responders given above, 18 subjects could be considered clinical responders to Interferon- $\alpha$ . The most relevant clinical, pathological and virological data of both groups are summarized in Table 2. Although the responder group contained more women and the non-responder group more men than theoretically expected, the observed imbalances were not significant ( $X^2$ -test). The duration of the disease in each subject was estimated based on anamnestic data (surgery with multiple transfusions, intravenous drug abuse, professional exposure through needle stick accident, etc.) or patient file data displaying chronically fluctuating and elevated transaminase levels. The disease duration varied from one to 32 years. The mean disease duration was  $9.2 \pm 9.2$  years in responders and  $6.8 \pm 5.4$  years in non-responders. Although the responder group contained more subjects treated with the experimental protocol and the non-responder group more subjects treated with the standard protocol, the imbalance was

not significant  $\chi^2$ -test). Twenty six out of 32 patients (81%) were infected with HCV of genotype 1b. The genotypes 3a, 4a and 5a were found in 4, 1 and 1 subject, respectively. Anamnestic data allowed us to retrieve the source of infection. Blood transfusions are the possible source of the HCV infection in 14 subjects, IV drug abuse in 3 patients and needle stick accidents in 3 others. No source of infection could be traced back in 12 subjects. Most patients (20 out of 32) showed pathological lesions compatible with chronic active hepatitis in a mild, moderate or severe form. Seven patients displayed signs of chronic persistent hepatitis. In two subjects the biopsy showed only aspecific lesions and in two others signs of liver cirrhosis were observed.

#### **Example 2. Analysis of the humoral immune response**

**[0104]** INNO-LIA HCV AbII (Innogenetics, Belgium) was employed to detect antibodies to peptide epitopes from the core, NS4a+b and NS5a region. From each patient a serum sample obtained before the start of the interferon therapy was examined and sometimes, additional follow-up samples were also tested. All 32 patients studied had circulating antibodies towards HCV demonstrated by two commercially available enzyme immunoassays. Using a peptide-based immunoblot assay (INNO-LIA HCV AbII) we were able to partially define the specificities of these antibodies. Sera from 31 patients were examined at least once with this assay and in 20 subjects the assay was applied on two sera taken with an interval of 4 (Patient 635) to 124 weeks (Patient 606). Table 3 shows the results of this survey. Apart from the reactivity pattern with the antigens employed (4 individually spotted core peptides, a mixture of NS4 peptides defining a fifth line and a selection of NS5 peptides creating a sixth line), Table 3 also shows the HCV genotype and the moment at which the serum was taken with respect to the start of the interferon therapy. The data clearly indicate that the antibody recognition pattern of an individual patient hardly changes over time. The only differences observed in the 20 paired samples were single step alterations in the intensity of the reactions. As well in responders as in non-responders to interferon we observed the same hierarchy in the serological reaction patterns. When indeterminate or weak reactions are not taken into consideration, the following hierarchy appears: Core2 > NS4 > NS5 > Core1 > Core4 > Core3.

#### **Example 3. Detection of HCV RNA and HCV genotyping**

**[0105]** Reverse transcription and PCR was performed as described previously (Stuyver et al, 1993). PCR products were further processed for genotyping by means of the Inno-LiPA genotyping assay (Stuyver et al., 1993). The results of the genotyping assays are included in Table 3.

#### **Example 4. Analysis of the cellular immune response**

##### **4.1. Synthesis of HCV antigens**

**[0106]** Nine groups of peptides (pools) corresponding to Core, E1 and E2/NS1 sequences, two single peptides not included in these pools corresponding to E2/NS1, and a recombinant protein representing the central part of NS3-HCV genotype 1b, were used for in vitro stimulation of PBMC. Each group pooled 4-6 different 20-mer peptides which overlapped 8 amino acids. Groups 1, 2 and 3 included mainly core peptides with amino acid positions 5-80, 73-140 and 133-200, respectively (Table 1). Groups 4, 5 and 6 predominantly encompassed E1 peptides with amino acid positions 193-260, 253-332 and 325-392, respectively. Groups 7, 8 and 9 comprised E2/NS1 peptides with amino acid positions 427-494, 487-578 and 571-638, respectively. The two additional single peptides (MS1-7\*, and NS1-5\*) covered amino acids from 397 to 428 of the E2 sequence (Table 1). A fusion protein containing the NS3 sequence was expressed in *E. coli* and covered HCV amino acids 1188 to 1463 of the Belgian isolate IG8309.

**[0107]** Peptides were dissolved in the buffers shown in Table 1 and added to the cultures at a final concentration of 10  $\mu\text{g/ml}$ . At this peptide concentration, the concentration of dissolving buffers in the cell cultures was not toxic or inhibitory. Preliminary experiments were performed to ascertain this. NS3 protein was used at a final concentration of 1.5  $\mu\text{g/ml}$ . Tetanus toxoid (WHO, Copenhagen, Denmark), used as a positive control antigen, was added to the culture media at a final concentration of 10  $\mu\text{g/ml}$ .

**[0108]** All the peptides were synthesized on either PepSyn K resin (Millipore) functionalized with the acid labile linker 4-( $\alpha$ -Fmoc-amino-2',4'-dimethoxybenzyl) phenoxyacetic acid, or TentaGel S-RAM resin (Rapp Polymere) functionalized with the same linker which yields peptide amides upon cleavage. *t*-Butyl-based side chain protection and Fmoc- $\alpha$ -amino protected amino acid derivatives were used. The guanidino group of arginine was 2,2,5,7,8-pentamethylchroman-6-sulfonyl-protected. The imidazole group of histidine was protected with either *t*-Boc or trityl and the sulfhydryl group of cysteine was protected with a trityl group. Couplings were carried out using preformed *O*-pentafluorophenyl esters except in the case of arginine where TBTU (*O*-(1*H*-benzotriazol-1-yl)-*N,N,N',N'*-tetramethyluronium tetrafluoroborate.; Novabiochem) was used as the activating agent in the presence of 2 equivalents of the base *N*-methylmorpholine and 1 equivalent of 1-hydroxybenzotriazole. Occasionally, glutamine, asparagine, and tryptophan were also

coupled using TBTU activation. In these cases, the trityl-protected derivatives of glutamine and asparagine (Millipore), and the t-Boc-protected derivative of tryptophan (Novabiochem) were used. All syntheses were carried out on a Milligen 9050 PepSynthesizer (Millipore) using continuous flow procedures. Following cleavage of the peptides with trifluoroacetic acid in the presence of appropriate scavengers and precipitation with diethylether, all peptides were analyzed by C<sub>18</sub>-reverse phase chromatography.

[0109] HCV amino acid sequences corresponding to the viral nucleocapsid (core) and E1 proteins were based on the HC-J1 sequence described by Okamoto *et al.* (1990) Japan. J. Exp. Med. (1990) 60:167-177. HCV sequences starting at amino acid residue Gly<sub>451</sub> were taken from the sequences reported by Choo *et al.* (1991) Proc. Natl. Acad. Sci. USA (1991) 88:2451-2455. Most peptide sequences were chosen such that the peptides would overlap each other by 8 amino acid residues.

#### 4.2. T cell proliferation assays

[0110] The medium used for all cell cultures consisted of RPMI 1640 supplemented with 25 mM HEPES, 2 mM L-glutamine, 50 U/ml penicillin and 50 µg/ml streptomycin (all from Gibco Europe, Gent, Belgium), 5×10<sup>-5</sup> M 2-mercaptoethanol (Sigma, St. Louis, Mo.) and 10% heat-inactivated pooled human AB serum. This AB serum was obtained from healthy blood donors with blood group AB<sup>+</sup> and was only used when antibodies to HCV and HCV-RNA were absent. This "complemented" RPMI 1640 medium will hereafter be designated "complete medium".

[0111] PBMC were isolated from heparinized venous blood by isopycnic density centrifugation on Ficoll Hypaque (Lymphoprep, Nyegaard, Denmark) and suspended in complete medium. 4×10<sup>5</sup> PBMC in 200 µl of complete medium were cultured in 96 well roundbottomed microplates (Falcon Plastics) in the absence (unstimulated controls) or presence of varying concentrations of antigens for 5 days at 37°C in an atmosphere of 5% CO<sub>2</sub> in air. 0.5 µCi (<sup>3</sup>H)-thymidine was then added to each well and 16 to 20 h later the cultures were harvested onto glass fiber filters using a multichannel cell harvester (PHD, Cambridge, MA) to measure the incorporation of (<sup>3</sup>H)-thymidine by liquid scintillation counting in an LKB-Wallac 8100 counter (LKB, Bromma, Sweden). Results are expressed as stimulation index (SI; mean cpm of antigen-stimulated cultures/mean cpm of control cultures). Proliferation was considered positive when stimulation index was >3. In some figures the results are expressed as cpm (mean cpm of antigen-stimulated cultures - mean cpm of control cultures). Standard deviations of the mean cpm of triplicate cultures were consistently below 10%.

[0112] The occurrence of *in vivo* primed HCV-specific memory T lymphocytes was examined using a lymphoproliferation assay. PBMC from 32 patients with chronic HCV were stimulated *in vitro* with pools of 4 to 6 partially overlapping, synthetic peptides representing the core, E1 and E2/NS1 regions of HCV type 1a, with 2 overlapping, single peptides from the amino-terminus of HCV type 1a and with a recombinant fusion protein containing the NS3 sequence of HCV type 1b. In all but 2 patients (#610 and #636) at least 2 and up to 11 (#633) assays were performed. In patient #632 for example lymphoproliferation was examined on 8 different occasions between week 4 and 54 following the start (week 0) of the Interferon therapy. Figure 1 shows the results of these assays in correlation with the biochemical (ALT/AST) response to therapy. Four weeks after the start of Intron-A (Schering Plough) a normalization of the transaminase levels was observed. PBMC's from the patient consistently and vigorously proliferate upon stimulation with peptide pools 2 and 3. The responses to the other antigen preparations were less vigorous and less reproducible, suggesting that the number of memory cells recognizing these epitopes is lower. Antigens that did not induce a proliferative response with a stimulation index (SI) 3 at any time are not represented in the graph.

[0113] To analyze and summarize the results of 135 assays performed in the 32 HCV patients, we have chosen to consider the response of an individual patient to a particular antigen preparation (peptide pools 1 to 9, NS1-5\*, NS1-7\* or NS3 protein) as significant when it induces SI's 3 in at least half of the assays performed. The results shown in Table 4 have been obtained using this scoring method. The Table shows the antigen recognition pattern of chronic HCV patients towards the 12 antigen preparations standardly used. Apart from the individual patient number and the number of assays performed with PBMC's from each subject, Table 4 also shows the time frame wherein these assays were executed. The start of the Interferon therapy serves as the reference point, week 0. None of the patients responded to all the antigens. PBMC's from 13 of 18 (72%) clinical responders and 12 of 14 (85%) non-responders proliferated in response to at least one antigen preparation. All but one antigen preparation, peptide pool 8, induced a proliferative response in at least one subject. The most frequent responses were to peptide pools 2 and 3. Whereas both interferon-responders and non-responders proliferated equally well to peptide pool 2 (56% and 57%, respectively), non-responders reacted less well to peptide pool 3 (29% or 4 of 14) than responders (44% or 8 of 18). Similar imbalances were observed for the reactions to peptide pools 5 and 9, that were more frequently recognized by non-responders (43% and 43%, respectively) than by responders (17% and 11%, respectively). Clinical non-responders to interferon therapy also reacted more frequently (57% or 8 of 14) upon stimulation with the NS3 protein than responders (24% or 4 of 17). However, none of these differences in proliferative response rates to peptide pools 3, 5 and 9 or to NS3 protein reached statistical significance (p<0.05 in <sup>2</sup>-test). A striking and significant difference (p=0.01 in <sup>2</sup>-test) was observed for the response rate of responders and non-responders to peptides NS1-5\* and NS1-7\*. Indeed, 8 of 17 responders recog-

nized one or both peptides while none of the non-responders did so. A summary of the results of all these proliferation assays is provided in Figure 2, in which the response rates of the HCV patients as well as 18 healthy control subjects towards the 12 antigen preparations. Indeed, to establish the relevance of the proliferative responses observed in HCV patients, PBMC's from 18 healthy control subjects were stimulated with the same antigen preparations. Overall, 27 assays were performed: a single assay in 10 subjects, two in 7 volunteers and 3 in one individual. In 12 control subjects none of the antigens induced a proliferative response. In 6 subjects one or more antigens induced a proliferative response with an SI 3 in a unique assay or in at least half of the assays performed. Table 5 shows the antigens that induced the proliferation in these subjects. Although Figure 2 suggests that proliferative responses occur more frequently in HCV patients than in healthy controls, these differences do not always reach statistical significance ( $p < 0.05$ ). Peptide pools 2 and 3 and the NS3 protein clearly ( $p < 0.05$ ) induce more frequent proliferative responses in the whole group of HCV patients than in healthy controls. Most of these differences are also significant when interferon responders and non-responders are each compared to the healthy control group. Only for the proliferative response to NS3 of interferon responders this is no longer valid. Although the frequency of proliferative response to peptide pool 5 in healthy controls and HCV patients were not significantly different, they turned out to be so ( $p < 0.03$ ) when only the non-responders were compared to the control subjects. All other differences did not reach the  $p < 0.05$  level.

**Example 5. Fine specificity of the recognition of the HCV core region by PBMC from clinical responders: T cell epitope localization in the core carboxyterminal region**

[0114] Since peptide pools 2 and 3 elicited proliferative responses in a large fraction of HCV patients, we have examined which peptides from these pools were inducing these responses. The stimulatory capacity of single peptides on PBMC's from healthy control subjects was tested as well. Twenty-three proliferation assays were performed with PBMC's from 17 control subjects. Peptides core C17, core C21 and core C31 were recognized by 2, 1 and 1 subject or 12%, 6% and 6% of subjects, respectively. PBMC's were prepared from 11 HCV patients that responded to interferon therapy. Eight subjects had displayed a proliferative response to either one or both peptide pools 2 and 3, whereas 3 patients had not. Nineteen assays were performed. The scoring system for positive reactions was as described in example 4. Table 6 summarizes the results of these 19 assays and demonstrates the consistency of the assay results. Indeed, PBMC's from the patients that had not reacted to the peptide pools did not proliferate upon stimulation with any of the individual peptides. The PBMC's from the patients that had displayed a proliferative response before, also reacted upon stimulation with one or several peptides from these pools. At least one and up to five of these peptides were recognized by these patients. The most immunogenic region of the HCV core sequence seems to be located between amino acids 109 and 176. Peptides C27 (AA 157-176), recognized by 6 of the 8 proliferative responders, turns out to be the most immunodominant one, followed by C25 which is recognized by 5 patients, and C23 and C19 which are recognized by 3 subjects.

**Example 6**

[0115] The fine specificity of the lymphoproliferative responses was tested again with new samples, the majority of which was obtained from other patients than those analyzed in example 5. Five patients (two  $\alpha$ IFN responders and three  $\alpha$ IFN non-responders) and 16 normal controls were examined. Table 7 shows the results of the assays performed in chronic hepatitis C patients. The highest LPR observed in both  $\alpha$ IFN responders tested was towards aa positions : 73-92 (C13); 109-128 (C19); 121-140 (C21); 145-164 (C25); 157-176 (C27). Only aa residues 121-140 (C21) and 133-152 (C23) elicited a high PLR in two  $\alpha$ IFN non-responders. Therefore, the use of peptides C13, C19, C25 and/or C27 in prophylactic or therapeutic vaccine compositions may be particularly advantageous.

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TABLE 1  
Synthetic peptides used as antigens in the lymphoproliferative assays.

HCV REGION	POOL	PEPTIDE NAME	AMINO ACID (AA) SEQUENCE	AA POSITION	SEQ ID NO	SOLVENT
CORE	1	CORE 2	PKPQRKTKRNTNRRP	5-19	1	A
		CORE 3	RNTNRRPQDVKFPQGGQIVG	13-32	2	A
		CORE 5	PGGGQIVGQVLLPBRPRL	25-44	3	B
		CORE 9	TRKTSERSQPRGRQPFKV	49-68	4	A
		CORE 11	RRQPFKVRPEORTWAQPG	61-80	5	A
	2	CORE 13	GRIWAQPGYPWLYGNEGCO	73-92	6	B
		CORE 15	LYGNEGCOGWAGWLLSPRGR	85-104	7	C
		CORE 17	LLSPRGRSPSWGPTDFRRS	99-116	8	A
		CORE 19	PTDFRRSRNLGKVIDILTC	109-128	9	A
		CORE 21	KVIDILTCGFADLMGYTLV	121-140	10	D
	3	CORE 23	LMGYTLVGAPLOGAARALA	133-152	11	A
		CORE 25	GGAAARALAHGVKVLDDVNY	145-164	12	A
		CORE 27	VLEDGVNYATONLPGCSFSI	157-176	13	E
		CORE 29	LPGCSFSIFLLALLSCLTVP	169-188	14	O
		CORE 31	LLSCLTVPASATQVRNSTGL	181-200	15	C
E1	4	E1-33	QVRNSTOLYHVINDCPNSSI	193-212	16	O
		E1-35	NDCPNSSIVYEARDAILHP	205-224	17	C
		E1-37	HDAIHIPGCVPCVREGNV8	217-236	18	A
		E1-39	CVREGNVSRGWVAMPTVAT	229-248	19	H
		E1-41	AMPTVATIRDOKLPATQLER	241-260	20	A
	5	E1-43	LPATQLRRHIDLVGSAITC	253-272	21	H
		E1-45	LVGSAITLCIALTVGDLGGSV	265-284	22	E
		E1-49	QLFIPSPRHHWTTCQNCIS	289-308	23	H
		E1-51	TQQCNCISYPOHITHGRMAW	301-320	24	B
		E1-53	ITGRMAWDMQAGNWSPTAAL	313-332	25	H
	6	E1-55	NWSPTAALVMAQLLRIPQAI	325-344	26	H
		E1-57	ILRRPQAILDMAGAHWGL	337-356	27	H
		E1-59	AGAHWGLVLAGIAYFSMVGNW	349-368	28	I
		E1-63	VVLLIFAGVDAEIVSGGQA	373-392	29	E
	E2/NSI	7	LNCRNSLNTOWWLAGLIYQK	427-446	30	C
			AGLIYQHKFNSOCERLAS	439-458	31	B
			GCERLASCRPLTDFDQGWG	451-470	32	B
			IDFDQGWGFISTANGSGPDQ	463-482	33	A
			ANGSGPDQRFYCYWHYPPKPC	475-494	34	A
		8	WHYPPKPGHIVAKSVCGPV	487-506	35	B
			AKSVCGPVYCFIPSPVVGT	499-518	36	O
			PSFVVGTIDRSGAPITYSWG	511-530	37	C
			GAPITYSWGENDIDVFLNNT	523-542	38	E
			QNWFGCTWQNSTGFIKVOGA	547-566	39	O
		9	GFIVGGAFFVCIGGAGNNT	559-578	40	A
			IGGAGNNTLHCPTDCFRKHP	571-590	41	A
			IDCFRKHFPDATTSCGSPFW	583-602	42	A
			SRGSGSPWIIIFCLVDYFYR	595-614	43	B
			CLVDYFYRLWHYFCTINYTI	607-626	44	C
			FCTINYTIKRMVVOOVER	619-638	45	A
			SGLVSLFIPGAKQNIQLNT	397-416	46	C
		NSI-5'	QNIQLDNTNGSWHNTALN	409-428	47	C

## Solvents used:

Solvent A: 0.1% trifluoroacetic acid; Solvent B: 0.1% trifluoroacetic acid, 25% acetonitrile; Solvent C: 0.1% trifluoroacetic acid, 30% acetonitrile; Solvent D: 0.1% trifluoroacetic acid, 50% acetonitrile; Solvent E: 0.005 ammonia buffer; Solvent O: 50% dimethyl sulfoxide; Solvent H: 0.1% trifluoroacetic acid, 40% acetonitrile.

Table 2. General data from HCV patients.

Patient	Gender	Age	AP Diagnosis	CLINICAL			RESPONDERS		
				Source	Duration (Years)	Genotype	IFN Scheme	ALT before therapy	
604	F	30	CAH: mod	IVDA	10	1b	2	150	5
607	M	39	CPH	Unknown	2	1b	1	182	10
608	M	61	CAH: mild	Transfusion	7	3a	1	196	
610	F	27	Non spec	Unknown	2	1b	2	219	
614	M	56	CAH: mild	Transfusion	10	1b	2	425	
615	M	71	CAH: mod	Unknown	2	1b	1	201	
616	F	52	Non spec	Transfusion	5	1b	1	152	
618	F	37	CPH	Needle stick	5	1b	2	60	
621	M	48	CAH: mod	Unknown	8	1b	1	63	
624	M	31	CPH	Needle stick	15	1b	2	158	
626	F	34	CAH: sev	Transfusion	6	3a	2	168	
630	M	30	CPH	Needle stick	5	1b	2	9	
632	M	57	CPH	Unknown	1	4a or 5a	2	359	
633	F	30	CAH: mod	Transfusion	2	1b	2	292	
634	F	67	CAH: mod	Unknown	32	1b	2	481	
635	F	47	prob cirrh	Transfusion	14	1b	2	100	
636	F	54	CAH: mod	Unknown	7	5a	1	90	
639	F	62	CAH	Transfusion	32	1b	1	79	
Patient	Gender	Age	AP Diagnosis	CLINICAL			NON-RESPONDERS		
				Source	Duration (Years)	Genotype	IFN Scheme	ALT before therapy	
601	M	32	CAH: mod	Transfusion	3	1b	2	141	
602	M	66	CAH: mod	Transfusion	3	1b	1	349	
603	M	45	CAH: sev	Transfusion	17	1b	2	157	
606	F	53	CAH: mod	Unknown	2	1b	1	299	
611	M	51	CPH	Transfusion	7	1b	1	195	
613	F	38	CAH: mod	IVDA	17	3a	1	178	

CAH = CHRONIC ACTIVE HEPATITIS. CPH = CHRONIC PERSISTENT HEPATITIS. CIRRH = CIRRHOSIS. NON SPEC = NOT DONE OR NOT SPECIFIC ABNORMALITIES

Table 2 continued. General data from HCV patients.

617	M	71	CAH: sev	Transfusion	3	1b	1	447
620	M	67	CAH: mod	Unknown	2	1b	1	138
622	M	40	CAH: sev	Transfusion	11	1b	1	291
625	M	70	CAH: mod	Unknown	1	1b	1	134
627	M	44	CAH: mod	IVDA	8	3a	1	254
629	F	61	Cirrh	Transfusion	11	1b	1	179
631	M	69	CPH	Unknown	5	1b	2	358
637	F	59	Cirrh	Unknown	5	1b	2	118

CAH = CHRONIC ACTIVE HEPATITIS. CPH = CHRONIC PERSISTENT HEPATITIS. CIRRH = CIRRHOSIS. NON SPEC = NOT DONE OR NOT SPECIFIC ABNORMALITIES

Table 3. Antibody reactivities to 6 HCV antigens of the Line Immuno-Assay in 32 chronic HCV patients.

CLINICAL Patient	Weeks	RESPONDERS						
		Genotype	NS4	NS5	C1	C2	C3	C4
604	-6	1b	3	3	2	2	-	-
	90		3	3	3	3	-	2
607	-11	1b	2	3	2	-	-	-
	84		3	3	3	-	-	-
608	-6	3a	-	3	-	-	-	-
610	-6	1b	3	-	2	3	-	-
614	30	1b	3	3	2	2	-	-
	60		2	3	3	3	-	-
615	-2	1b	3	-	-	2	-	-
616	-6	1b	3	-	2	3	2	2
618	-6	1b	-	-	-	3	-	-
	54		-	-	-	2	-	-
621	-3	1b	3	3	2	-	-	-
	30		3	3	2	-	-	-
624	-5	1b	3	3	2	2	-	-
	20		3	3	2	3	2	2
626	2	3a	-	2	2	3	-	-
	20		2	2	3	3	-	2
630	-12	1b	3	-	2	2	-	-
	8		3	-	2	2	-	-
632	-6	4a or 5a	-	-	2	3	2	2
	8		-	3	2	3	2	2
633	-6	1b	3	3	-	2	-	2

"-" denotes negative, indeterminate or weak reactions. 2, moderate reaction. 3, strong reaction.

Table 4. T-cell recognition of 12 HCV antigens in 32 chronic hepatitis C patients under alpha-interferon therapy.

CLINICAL		RESPONDERS													
Patient	Genotype	N°. Assays	Time of assays	P1	P2	P3	P4	P5	P6	P7	P8	P9	NS1-7*	NS1-5*	NS3
604	1b	2	w90-108		+	+	+	+	+			+	+	+	+
607	1b	2	w84-120		+							+	+	+	ND
608	3a	2	w90-108		+	+						+	+	+	+
610	1b	1	w84										ND		
614	1b	4	w60-108												
615	1b	2	w66-84	+	+	+	+	+						+	+
616	1b	3	w78-108											+	+
618	1b	4	w54-84	+	+									+	+
621	1b	4	w30-60			+						+	+	+	
624	1b	9	w20-90		+	+									
626	3a	9	w16-60		+	+							+		
630	1b	6	w8-75												
632	4a or 5a	8	w4-54		+	+									
633	1b	11	w0-48												
634	1b	3	w0-24		+										
635	1b	7	w6-54											+	+
636	5a	1	w24		+	+								+	+
639	1b	4	w3-19	+	+	+							+	+	
CLINICAL		NON-RESPONDERS													
Patient	Genotype	N°. Assays	Time of assays	P1	P2	P3	P4	P5	P6	P7	P8	P9	NS1-7*	NS1-5*	NS3
601	1b	4	w90-140		+	+	+	+	+			+			+
602	1b	2	w96-108		+	+	+					+			+
603	1b	2	w78-93		+	+	+	+				+			+
606	1b	3	w84-96		+	+	+	+				+			+
611	1b	2	w66-84		+			+				+			+
613	3a	8	w60-96		+	+		+				+			+
617	1b	5	w60-108												
620	1b	3	w42-66					+				+			+
622	1b	3	w30-54									+			+
625	1b	4	w20-66		+	+						+			+
627	3a	3	w16-24		+							+			+
629	1b	2	w20-48		+		+					+			+
631	1b	5	w4-w16	+	+		+	+		+		+			+
637	1b	7	w6-16			+									

P1-3 corresponds to Core, P4-6 represents E1, P7-9 comprises E2/NS1. (+) denotes lymphoproliferative response. ND- Not done.

Table 5. Antigens recognized by 6 control subjects displaying significant \* lymphoproliferation responses.

SUBJECTS	N° ASSAYS	P1	P2	P3	P4	P5	P6	P7	P8	P9	NS1-7*	NS1-5*	NS3
CAE	3										+		
IDS	1		+										+
LCE	1											+	
MVH	1		+		+	+				+		+	
PDG	2				+								
RDB	2		+		+								

\* A response is considered significant when a S.I. equal or greater than 3 in a single peptide assay or in at least half of the assays performed.



Table 6. The lymphoproliferative responses to peptide pools are consistent with lymphoproliferative responses to single peptides fr.

		PEPTIDE POOLS								SINGLE				PEPTIDES					
		N° assays	Pool 2	Pool 3						P2									
	Patient																P3		
	604	2	+	+											+		-	-	-
	615	2	+	+											+		+	-	-
	618	4	+	-											-		+	-	-
	621	4	-	+											-		+	-	-
	626	9	+	+											-		+	-	-
	632	8	+	+											+		+	-	-
	634	2	+	-											-		+	-	-
	639	4	+	+											-		+	-	+

Table 7.

Fine specificity of T-cell recognition of P2 and P3 Core individual peptides.

Patient N°	Clinical response to $\alpha$ IFN <sup>a</sup>	Week <sup>b</sup>	Blank <sup>c</sup>	TT <sup>d</sup>	P2 peptides							P3 peptides		
					C13 <sup>e</sup>	C15	C17	C19	C21	C23	C25	C27	C29	C31
626	R	14	750	14.5	4.4	-	-	-	3.3	-	6	8.2	-	-
636	R	28	1032	3.6	6.3	-	-	7.1	-	-	9.7	5.8	-	-
620	NR	20	5047	4.1	ND <sup>f</sup>	ND	ND	ND	ND	4.1	-	-	-	-
627	NR	54	928	19.1	-	-	-	-	3.6	-	-	-	-	-
637	NR	45	2370	4.2	-	-	-	-	-	-	-	-	-	-

<sup>a</sup> R: responder; NR: Not responder.<sup>b</sup> Time points of  $\alpha$ IFN therapy on which LPA were performed.<sup>c</sup> Values express cpm.<sup>d</sup> TT: Tetanus toxoid. Values denote SI.<sup>e</sup> C13-C21 and C23-C31 are the individual peptides of P2 and P3 Core peptide pools. Only SI equal or greater than 3 are shown.<sup>f</sup> ND: Not done.

## SEQUENCE LISTING

[0150]

## 5 (1) GENERAL INFORMATION:

## (i) APPLICANT:

10 (A) NAME: Innogenetics s.a.  
 (B) STREET: Industriepark Zwijnaarde 7, box 4  
 (C) CITY: Ghent  
 (B) COUNTRY: Belgium  
 (F) POSTAL CODE (ZIP): B-9052  
 (G) TELEPHONE: 00 32 9 241 07 11  
 15 (H) TELEFAX: 00 32 9 241 07 99

(ii) TITLE OF INVENTION: Immunodominant human T cell epitopes of Hepatitis C virus structural proteins,  
 prophylactic and therapeutic compositions containing the same

20 (iii) NUMBER OF SEQUENCES: 166

## (iv) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## 30 (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro  
 1 5 10 15

45

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly  
 1 5 10 15  
 5 Gln Ile Val Gly  
 20

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg  
 1 5 10 15  
 25 Gly Pro Arg Leu  
 20

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS;

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 1 5 10 15  
 45 Ile Pro Lys Val  
 20

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Arg Arg Gln Pro Ile Pro Lys Val Arg Arg Pro Glu Gly Arg Thr Trp  
 1 5 10 15

5 Ala Gln Pro Gly  
 20

(2) INFORMATION FOR SEQ ID NO: 6:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn  
 1 5 10 15  
 25 Glu Gly Cys Gly  
 20

(2) INFORMATION FOR SEQ ID NO: 7:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro  
 1 5 10 15  
 45 Arg Gly Ser Arg  
 20

(2) INFORMATION FOR SEQ ID NO: 8:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
1                      5                      10                      15

Arg Arg Arg Ser  
                20

(2) INFORMATION FOR SEQ ID NO: 9:

10

(i) **SEQUENCE CHARACTERISTICS:**

15 (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp  
1                      5                      10                      15

Thr Leu Thr Cys  
                20

(2) INFORMATION FOR SEQ ID NO: 10:

30

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

45

Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr  
1 5 10 15  
Ile Pro Leu Val  
20

(2) INFORMATION FOR SEQ ID NO: 11:

50

(i) **SEQUENCE CHARACTERISTICS:**

55 (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

5           Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala  
          1                               5                               10                               15  
          Arg Ala Leu Ala  
  20

10       (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

15       (A) LENGTH: 20 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

20       (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

25           Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
          1                               5                               10                               15  
          Gly Val Asn Tyr  
  20

30       (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

35       (A) LENGTH: 20 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

40       (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

45           Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys  
          1                               5                               10                               15  
          Ser Phe Ser Ile  
  20

50       (2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

55       (A) LENGTH: 20 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

5

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys  
1 5 10 15

Leu Thr Val Pro  
20

10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn  
1 5 10 15

Ser Thr Gly Leu  
20

30

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

45

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro  
1 5 10 15

Asn Ser Ser Ile  
20

50

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

5

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile  
 1 5 10 15

10

Leu His Thr Pro  
 20

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25

His Asp Ala Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu  
 1 5 10 15

30

Gly Asn Val Ser  
 20

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

45

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro  
 1 5 10 15

50

Thr Val Ala Thr  
 20

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

5

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Pro Ala  
1 5 10 15

Thr Gln Leu Arg Arg  
20

10

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

25

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
1 5 10 15

Ala Thr Leu Cys  
20

30

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

45

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu  
1 5 10 15

Cys Gly Ser Val  
20

50

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION; SEQ ID NO: 23:

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys  
 1 5 10 15  
 Asn Cys Ser Ile  
 20

10

(2) INFORMATION FOR SEQ ID NO: 24:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His  
 1 5 10 15  
 Arg Met Ala Trp  
 20

30

(2) INFORMATION FOR SEQ ID NO: 25:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro  
 1 5 10 15  
 Thr Ala Ala Leu  
 20

50

(2) INFORMATION FOR SEQ ID NO: 26:

55

(i) SEQUENCE CHARACTERISTICS;

(A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile  
1 5 10 15  
Pro Gln Ala Ile  
20

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His  
1 5 10 15  
Trp Gly Val Leu  
20

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Phe Ser Met  
1 5 10 15  
Val Gly Asn Met  
20

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

EP 0 725 824 B1

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

10

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser  
1 5 10 15  
Gly Gly Gln Ala  
20

15

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

30

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Leu Ala Gly Leu Ile  
1 5 10 15  
Tyr Gln His Lys  
20

35

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

50

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu  
1 5 10 15  
Arg Leu Ala Ser  
20

55

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

EP 0 725 824 B1

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

10

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp  
1 5 10 15

Gln Gly Trp Gly  
20

15

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

30

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser  
1 5 10 15

Gly Pro Asp Gln  
20

35

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

50

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro  
1 5 10 15

Pro Lys Pro Cys  
20

55

(2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val  
 1 5 10 15  
 Cys Gly Pro Val  
 20

## (2) INFORMATION FOR SEQ ID NO: 36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val  
 1 5 10 15  
 Val Val Gly Thr  
 20

## (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr  
 1 5 10 15  
 Tyr Ser Trp Gly  
 20

## (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

15 Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys  
 1 5 10 15  
 Asn Cys Ser Ile  
 20

20

## (2) INFORMATION FOR SEQ ID NO: 39:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

35 Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys  
 1 5 10 15  
 Val Cys Gly Ala  
 20

40

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

55 Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Cys Val Ile Gly Gly Ala  
 1 5 10 15  
 Gly Asn Asn Thr  
 20



## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

15 Ile Gly Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Phe  
 1 5 10 15  
 Arg Lys His Pro  
 20

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

35 Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly  
 1 5 10 15  
 Ser Gly Pro Trp  
 20

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

55

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp  
 1 5 10 15

5 Tyr Pro Tyr Arg  
 20

(2) INFORMATION FOR SEQ ID NO: 44:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile  
 1 5 10 15  
 25 Asn Tyr Thr Ile  
 20

(2) INFORMATION FOR SEQ ID NO: 45:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly  
 1 5 10 15  
 45 Gly Val Glu His  
 20

(2) INFORMATION FOR SEQ ID NO: 46:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

5           Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln  
          1                           5                           10                           15  
          Leu Ile Asn Thr  
                          20

10       (2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

15           (A) LENGTH: 20 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

20       (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

25           Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn Ser  
          1                           5                           10                           15  
          Thr Ala Leu Asn  
                          20

30       (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

35           (A) LENGTH: 68 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

40       (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

45           (A) NAME/KEY: misc-feature  
          (B) LOCATION: 1  
          (D) OTHER INFORMATION: Xaa is Pro or Gln

(ix) FEATURE:

50           (A) NAME/KEY: misc-feature  
          (B) LOCATION: 2  
          (D) OTHER INFORMATION: Xaa is Asn or Thr

(ix) FEATURE:

55           (A) NAME/KEY: misc-feature  
          (B) LOCATION: 6  
          (D) OTHER INFORMATION: Xaa is Arg or His

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: Xaa is Arg or Lys

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 11
- (D) OTHER INFORMATION: Xaa is Leu or Val or Phe

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 13
- (D) OTHER INFORMATION: Xaa is Lys or Arg

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 18
- (D) OTHER INFORMATION: Xaa is Leu or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 22
- (D) OTHER INFORMATION: Xaa is Phe or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 26
- (D) OTHER INFORMATION: Xaa is Met or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 27
- (D) OTHER INFORMATION: Xaa is Gly or Glu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 31
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 32
- (D) OTHER INFORMATION: Xaa is Val or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 34

(D) OTHER INFORMATION: Xaa is Ala or Gly

(ix) FEATURE:

- 5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 36  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- 10 (A) NAME/KEY: misc-feature  
(B) LOCATION: 39  
(D) OTHER INFORMATION: Xaa is Ala or Val

(ix) FEATURE:

- 15 (A) NAME/KEY: misc-feature  
(B) LOCATION: 40  
(D) OTHER INFORMATION: Xaa is Ala or Ser

(ix) FEATURE:

- 20 (A) NAME/KEY: misc-feature  
(B) LOCATION: 41  
(D) OTHER INFORMATION: Xaa is Arg or Ala

(ix) FEATURE:

- 25 (A) NAME/KEY: misc-feature  
(B) LOCATION: 42  
(D) OTHER INFORMATION: Xaa is Ala or Thr or Glu

(ix) FEATURE:

- 30 (A) NAME/KEY: misc-feature  
(B) LOCATION: 44  
(D) OTHER INFORMATION: Xaa is Ala or Glu

(ix) FEATURE:

- 35 (A) NAME/KEY: misc-feature  
(B) LOCATION: 49  
(D) OTHER INFORMATION: Xaa is Val or Ala or Leu

(ix) FEATURE:

- 40 (A) NAME/KEY: misc-feature  
(B) LOCATION: 50  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- 45 (A) NAME/KEY: misc-feature  
(B) LOCATION: 51  
(D) OTHER INFORMATION: Xaa is Glu or Gly

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 54
- (D) OTHER INFORMATION: Xaa is Val or Ile

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 56
- (D) OTHER INFORMATION: Xaa is Phe or Tyr

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 57
- (D) OTHER INFORMATION: Xaa is Ala or Pro

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 61
- (D) OTHER INFORMATION: Xaa is Leu or lie

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

25

```

Xaa Xaa Asp Pro Arg Xaa Xaa Ser Arg Asn Xaa Gly Xaa Val Ile Asp
1          5          10          15
Thr Xaa Thr Cys Gly Xaa Ala Asp Leu Xaa Xaa Tyr Ile Pro Xaa Xaa
20          25          30
Gly Xaa Pro Xaa Gly Gly Xaa Xaa Xaa Xaa Leu Xaa His Gly Val Arg
35          40          45
Xaa Xaa Xaa Asp Gly Xaa Asn Xaa Xaa Thr Gly Asn Xaa Pro Gly Cys
50          55          60
Ser Phe Ser Ile
65
  
```

35

(2) INFORMATION FOR SEQ ID NO: 49:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Ser or Ala or Gln or Leu or Asn or Tyr or Arg or His

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature

EP 0 725 824 B1

(B) LOCATION: 2

(D) OTHER INFORMATION: Xaa is Gly or Ser or Thr or Ala or Arg

(ix) FEATURE:

5

(A) NAME/KEY: misc-feature

(B) LOCATION: 3

(D) OTHER INFORMATION: Xaa is Phe or Ile or Leu or Val

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 4

(D) OTHER INFORMATION: Xaa is Val or Ala or Thr

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 5

(D) OTHER INFORMATION: Xaa is Ser or Asp or Gly

20

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 6

(D) OTHER INFORMATION: Xaa is Leu or Ile or Trp or Phe or Met

25

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 7

(D) OTHER INFORMATION: Xaa is Leu or Ile or Phe

30

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 8

(D) OTHER INFORMATION: Xaa is Ala or Thr or Asp or Ser

35

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 9

(D) OTHER INFORMATION: Xaa is Pro or Gln or Ser or Arg or Leu or Ile or Thr

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 11

(D) OTHER INFORMATION: Xaa is Ala or Pro or Ser

50

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 12

(D) OTHER INFORMATION: Xaa is Lys or Ser or Gln or Ala or Arg

55

(ix) FEATURE:

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- (A) NAME/KEY: misc-feature  
(B) LOCATION: 14  
(D) OTHER INFORMATION: Xaa is Asn or Lys or Asp or Arg

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Val or Ile or Leu

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 16  
(D) OTHER INFORMATION: Xaa is Gln or Ser or Tyr

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 18  
(D) OTHER INFORMATION: Xaa is Ile or Val

20

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 20  
(D) OTHER INFORMATION: Xaa is Thr or Ser

25

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 26  
(D) OTHER INFORMATION: Xaa is Leu or Ile

30

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 28  
(D) OTHER INFORMATION: Xaa is Ser or Arg

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Xaa Xaa Xaa  
1 5 10 15  
Leu Xaa Asn Xaa Asn Gly Ser Trp His Xaa Asn Xaa Thr Ala Leu Asn  
20 25 30

45

50 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

55



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Met or Ile

(ix) FEATURE:

10 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Gly or Glu

(ix) FEATURE:

15 (A) NAME/KEY: misc-feature  
(B) LOCATION: 7  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

20 (ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
25 (D) OTHER INFORMATION: Xaa is Val or Leu

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
30 (B) LOCATION: 10  
(D) OTHER INFORMATION: Xaa is Ala or Gly

(ix) FEATURE:

35 (A) NAME/KEY: misc-feature  
(B) LOCATION: 12  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

40 (A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Ala or Val

(ix) FEATURE:

45 (A) NAME/KEY: misc-feature  
(B) LOCATION: 16  
(D) OTHER INFORMATION: Xaa is Ala or Ser

50 (ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 17  
55 (D) OTHER INFORMATION: Xaa is Arg or Ala

(ix) FEATURE:

**EP 0 725 824 B1**

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 18
- (D) OTHER INFORMATION: Xaa is Ala or Thr or Glu

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 20
- (D) OTHER INFORMATION: Xaa is Ala or Glu

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 25
- (D) OTHER INFORMATION: Xaa is Val or Ala or Leu

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 26
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

20

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 27
- (D) OTHER INFORMATION: Xaa is Glu or Gly

25

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 30
- (D) OTHER INFORMATION: Xaa is Val or Ile

30

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 32
- (D) OTHER INFORMATION: Xaa is Phe or Tyr

35

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 33
- (D) OTHER INFORMATION: Xaa is Ala or Pro

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 37
- (D) OTHER INFORMATION: Xaa is Leu or Ile

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

55

1 Leu Xaa Xaa Tyr Ile Pro Xaa Xaa Gly Xaa Pro Xaa Gly Gly Xaa Xaa  
 5 Xaa Xaa Leu Xaa His Gly Val Arg Xaa Xaa Xaa Asp Gly Xaa Asn Xaa  
 Xaa Thr Gly Asn Xaa Pro Gly Cys Ser Phe Ser Ile  
 35 40

10 (2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20

(ix) FEATURE:

25 (A) NAME/KEY: misc-feature  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: Xaa is Val or Ala or Leu

(ix) FEATURE:

30 (A) NAME/KEY: misc-feature  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

35 (A) NAME/KEY: misc-feature  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: Xaa is Glu or Gly

(ix) FEATURE:

40

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: Xaa is Val or Ile

(ix) FEATURE:

45

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: Xaa is Phe or Tyr

(ix) FEATURE:

50

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: Xaa is Ala or Pro

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 13
- (D) OTHER INFORMATION: Xaa is Leu or Ile

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Xaa Xaa Xaa Asp Gly Xaa Asn Xaa Xaa Thr Gly Asn Xaa Pro Gly Cys  
 1 5 10 15  
 Ser Phe Ser Ile  
 20

15 (2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Ala or Val

30 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Ala or Ser

35 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Arg or Ala

40 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: Xaa is Ala or Thr or Glu

45 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: Xaa is Ala or Glu

50 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 13

(D) OTHER INFORMATION: Xaa is Val or Ala or Leu

(ix) FEATURE:

5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 14  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

10 (A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Glu or Gly

(ix) FEATURE:

15 (A) NAME/KEY: misc-feature  
(B) LOCATION: 18  
(D) OTHER INFORMATION: Xaa is Val or Ile

(ix) FEATURE:

20 (A) NAME/KEY: misc-feature  
(B) LOCATION: 20  
(D) OTHER INFORMATION: Xaa is Phe or Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

30 Xaa Xaa Xaa Asp Gly Xaa Asn Xaa Xaa Thr Gly Asn Xaa Pro Gly Cys  
1 5 10 15  
Ser Phe Ser Ile  
20

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

50 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Met or Ile

(ix) FEATURE:

55 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Gly or Glu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: Xaa is Val or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 10
- (D) OTHER INFORMATION: Xaa is Ala or Gly

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 12
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 15
- (D) OTHER INFORMATION: Xaa is Ala or Val

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 16
- (D) OTHER INFORMATION: Xaa is Ala or Ser

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 17
- (D) OTHER INFORMATION: Xaa is Arg or Ala

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 18
- (D) OTHER INFORMATION: Xaa is Ala or Thr or Glu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 20
- (D) OTHER INFORMATION: Xaa is Ala or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Leu Xaa Xaa Tyr Ile Pro Xaa Xaa Gly Xaa Pro Xaa Gly Gly Xaa Xaa  
 1 5 10 15

5 Xaa Xaa Leu Xaa  
 20

(2) INFORMATION FOR SEQ ID NO: 54:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 20 (A) NAME/KEY: misc-feature  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: Xaa is Pro or Gln

25 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: Xaa is Asn or Thr

30 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 6  
 35 (D) OTHER INFORMATION: Xaa is Arg or His

(ix) FEATURE:

- 40 (A) NAME/KEY: misc-feature  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: Xaa is Arg or Lys

(ix) FEATURE:

- 45 (A) NAME/KEY: misc-feature  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: Xaa is Leu or Val or Phe

(ix) FEATURE:

- 50 (A) NAME/KEY: misc-feature  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: Xaa is Lys or Arg

55 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 18

(D) OTHER INFORMATION: Xaa is Leu or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

5

Xaa Xaa Asp Pro Arg Xaa Xaa Ser Arg Asn Xaa Gly Xaa Val Ile Asp  
1 5 10 15

Thr Xaa Thr Cys  
20

10

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Ser or Ala or Gln or Leu or Asn or Tyr or Arg or His

(ix) FEATURE:

30

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Gly or Ser or Thr or Ala or Arg

35

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Phe or Ile or Leu or Val

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Val or Ala or Thr

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Ser or Asp or Gly

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: Xaa is Leu or Ile or Trp or Phe or Met

55



(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 7  
(D) OTHER INFORMATION: Xaa is Leu or Ile or Phe

5

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Ala or Thr or Asp or Ser

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 9  
(D) OTHER INFORMATION: Xaa is Pro or Gln or Ser or Arg or Leu or Ile or Thr

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 11  
(D) OTHER INFORMATION: Xaa is Ala or Pro or Ser

20

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 12  
(D) OTHER INFORMATION: Xaa is Lys or Ser or Gln or Ala or Arg

25

30

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 14  
(D) OTHER INFORMATION: Xaa is Asn or Lys or Asp or Arg

35

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Val or Ile or Leu

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 16  
(D) OTHER INFORMATION: Xaa is Gln or Ser or Tyr

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 18  
(D) OTHER INFORMATION: Xaa is Ile or Val

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 20

55

(D) OTHER INFORMATION: Xaa is Thr or Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

5 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Xaa Xaa Xaa  
1 5 10 15  
Leu Xaa Asn Xaa  
20

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDBDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Asn or Lys or Asp or Arg

(ix) FEATURE:

30 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Val or Ile or Leu

(ix) FEATURE:

35 (A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is Gln or Ser or Tyr

(ix) FEATURE:

40 (A) NAME/KEY: misc-feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: Xaa is Ile or Val

(ix) FEATURE:

45 (A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Thr or Ser

(ix) FEATURE:

50 (A) NAME/KEY: misc-feature  
(B) LOCATION: 14  
(D) OTHER INFORMATION: Xaa is Leu or Ile

## (ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 16

(D) OTHER INFORMATION: Xaa is Ser or Arg

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Gln Xaa Xaa Xaa Leu Xaa Asn Xaa Asn Gly Ser Trp His Xaa Asn Xaa  
 1 5 10 15  
 Thr Ala Leu Asn  
 20

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr  
 1 5 10 15  
 Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val  
 20 25 30  
 Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly  
 35 40 45  
 Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val  
 50 55 60  
 Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr  
 65 70 75 80  
 Met Ser Lys Ala His Gly Val Asp Pro Asn Ile Arg Thr Gly Val Arg  
 85 90 95  
 Thr Ile Thr Thr Gly Ala Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe  
 100 105 110  
 Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys  
 115 120 125  
 Asp Glu Cys His Ser Ile Asp Ser Thr Ser Ile Leu Gly Ile Gly Thr  
 130 135 140  
 Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala  
 145 150 155 160  
 Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu  
 165 170 175

Glu Val Ala Leu Ser Ser Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala  
 180 185 190  
 5 Ile Pro Ile Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys His  
 195 200 205  
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Phe Gly  
 210 215 220  
 10 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro  
 225 230 235 240  
 Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly  
 245 250 255  
 15 Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr  
 260 265 270  
 Gln Thr Val Asp Phe Ser  
 275

20

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

35

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Arg or Lys

## (ix) FEATURE:

40

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Ala or Ser or Thr

## (ix) FEATURE:

45

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Ala or Gly

50

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: Xaa is Gln or Lys or Arg

55

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature

(B) LOCATION: 9  
(D) OTHER INFORMATION: Xaa is Tyr or His

(ix) FEATURE:

5

(A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Gly or Ala

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 17  
(D) OTHER INFORMATION: Xaa is Glu or Lys

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 19  
(D) OTHER INFORMATION: Xaa is Cys or Met or Leu

20

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 21  
(D) OTHER INFORMATION: Xaa is Trp or Leu

25

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 34  
(D) OTHER INFORMATION: Xaa is Ser or Asn or Thr or Asp or His

30

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 37  
(D) OTHER INFORMATION: Xaa is Pro or Gin

35

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 38  
(D) OTHER INFORMATION: Xaa is Asn or Thr

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 42  
(D) OTHER INFORMATION: Xaa is Arg or His

45

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 43  
(D) OTHER INFORMATION: Xaa is Arg or Lys

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 47
- (D) OTHER INFORMATION: Xaa is Leu or Val or Phe

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 49
- (D) OTHER INFORMATION: Xaa is Lys or Arg

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 54
- (D) OTHER INFORMATION: Xaa is Leu or Ile

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 58
- (D) OTHER INFORMATION: Xaa is Phe or Leu

20

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 62
- (D) OTHER INFORMATION: Xaa is Met or Ile

25

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 63
- (D) OTHER INFORMATION: Xaa is Gly or Glu

30

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 67
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

35

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 68
- (D) OTHER INFORMATION: Xaa is Val or Leu

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 70
- (D) OTHER INFORMATION: Xaa is Ala or Gly

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 72
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 75
- (D) OTHER INFORMATION: Xaa is Ala or Val

5

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 76
- (D) OTHER INFORMATION: Xaa is Ala or Ser

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 77
- (D) OTHER INFORMATION: Xaa is Arg or Ala

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 78
- (D) OTHER INFORMATION: Xaa is Ala or Thr or Glu

20

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 80
- (D) OTHER INFORMATION: Xaa is Ala or Glu

25

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 85
- (D) OTHER INFORMATION: Xaa is Val or Ala or Leu

30

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 86
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 87
- (D) OTHER INFORMATION: Xaa is Glu or Gly

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 90
- (D) OTHER INFORMATION: Xaa is Val or Ile

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 92

55

(D) OTHER INFORMATION: Xaa is Phe or Tyr

(ix) FEATURE:

- 5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 93  
(D) OTHER INFORMATION: Xaa is Ala or Pro

(ix) FEATURE:

- 10 (A) NAME/KEY: misc-feature  
(B) LOCATION: 97  
(D) OTHER INFORMATION: Xaa is Leu or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Gly Xaa Xaa Trp Xaa Xaa Pro Gly Xaa Pro Trp Pro Leu Tyr Xaa Asn  
 1 5 10 15  
 Xaa Gly Xaa Gly Xaa Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg  
 20 20 25 30  
 Pro Xaa Trp Gly Xaa Xaa Asp Pro Arg Xaa Xaa Ser Arg Asn Xaa Gly  
 35 40 45  
 Xaa Val Ile Asp Thr Xaa Thr Cys Gly Xaa Ala Asp Leu Xaa Xaa Tyr  
 50 55 60  
 Ile Pro Xaa Xaa Gly Xaa Pro Xaa Gly Gly Xaa Xaa Xaa Xaa Leu Xaa  
 65 70 75 80  
 His Gly Val Arg Xaa Xaa Xaa Asp Gly Xaa Asn Xaa Xaa Thr Gly Asn  
 85 90 95  
 Xaa Pro Gly Cys Ser Phe Ser Ile  
 100

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 45 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
50 (D) OTHER INFORMATION: Xaa is Arg or Lys

(ix) FEATURE:

- 55 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Ala or Ser or Thr

(ix) FEATURE:



- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Ala or Gly

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: Xaa is Gln or Lys or Arg

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: Xaa is Tyr or His

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 15
- (D) OTHER INFORMATION: Xaa is Gly or Ala

20

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 17
- (D) OTHER INFORMATION: Xaa is Glu or Lys

25

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 19
- (D) OTHER INFORMATION: Xaa is Cys or Met or Leu

30

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 21
- (D) OTHER INFORMATION: Xaa is Trp or Leu

35

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 34
- (D) OTHER INFORMATION: Xaa is Ser or Asn or Thr or Asp or His

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 37
- (D) OTHER INFORMATION: Xaa is Pro or Gln

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 38
- (D) OTHER INFORMATION: Xaa is Asn or Thr

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 42  
(D) OTHER INFORMATION: Xaa is Arg or His

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 43  
(D) OTHER INFORMATION: Xaa is Arg or Lys

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 47  
(D) OTHER INFORMATION: Xaa is Leu or Val or Phe

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 49  
(D) OTHER INFORMATION: Xaa is Lys or Arg

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 54  
(D) OTHER INFORMATION: Xaa is Leu or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 58  
(D) OTHER INFORMATION: Xaa is Phe or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 62  
(D) OTHER INFORMATION: Xaa is Met or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 63  
(D) OTHER INFORMATION: Xaa is Gly or Glu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 67  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 68

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(D) OTHER INFORMATION: Xaa is Val or Leu

(ix) FEATURE:

5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 70  
(D) OTHER INFORMATION: Xaa is Ala or Gly

(ix) FEATURE:

10 (A) NAME/KEY: misc-feature  
(B) LOCATION: 72  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

15 (A) NAME/KEY: misc-feature  
(B) LOCATION: 75  
(D) OTHER INFORMATION: Xaa is Ala or Val

(ix) FEATURE:

20 (A) NAME/KEY: misc-feature  
(B) LOCATION: 76  
(D) OTHER INFORMATION: Xaa is Ala or Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

30 Gly Xaa Xaa Trp Xaa Xaa Pro Gly Xaa Pro Trp Pro Leu Tyr Xaa Asn  
1 5 10 15  
Xaa Gly Xaa Gly Xaa Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg  
20 25 30  
35 Pro Xaa Trp Gly Xaa Xaa Asp Pro Arg Xaa Xaa Ser Arg Asn Xaa Gly  
35 40 45  
Xaa Val Ile Asp Thr Xaa Thr Cys Gly Xaa Ala Asp Leu Xaa Xaa Tyr  
50 55 60  
40 Ile Pro Xaa Xaa Gly Xaa Pro Xaa Gly Gly Xaa Xaa  
65 70 75

(2) INFORMATION FOR SEQ ID NO: 60:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

55 (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Val or Ile

## (ix) FEATURE:

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: Xaa is Phe or Tyr

## (ix) FEATURE:

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: Xaa is Ala or Pro

## (ix) FEATURE:

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: Xaa is Leu or Ile

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Xaa Asn Xaa Xaa Thr Gly Asn Xaa Pro Gly Cys Ser Phe Ser Ile  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: Xaa is Phe or Leu

## (ix) FEATURE:

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: Xaa is Met or Ile

## (ix) FEATURE:

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: Xaa is Gly or Glu

## (ix) FEATURE:

(A) NAME/KEY: misc-feature  
 (B) LOCATION: 11

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(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 12  
(D) OTHER INFORMATION: Xaa is Val or Leu

(ix) FEATURE:

10 (A) NAME/KEY: misc-feature  
(B) LOCATION: 14  
(D) OTHER INFORMATION: Xaa is Ala or Gly

(ix) FEATURE:

15 (A) NAME/KEY: misc-feature  
(B) LOCATION: 16  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

25 Gly Xaa Ala Asp Leu Xaa Xaa Tyr Ile Pro Xaa Xaa Gly Xaa Pro Xaa  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 62:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRAHDENESS: single  
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

40 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Met or Ile

(ix) FEATURE:

45 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Gly or Glu

50 (ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 7  
55 (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Val or Leu

5 (ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 10  
(D) OTHER INFORMATION: Xaa is Ala or Gly

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 12  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Ala or Val

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

25

Gly	Xaa	Ala	Asp	Leu	Xaa	Xaa	Tyr	Ile	Pro	Xaa	Xaa	Gly	Xaa	Pro	Xaa
1				5					10					15	

30

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Met or Ile

45

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Gly or Glu

50

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: Xaa is Val or Leu

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: Xaa is Ala or Gly

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 11
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

15

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 14
- (D) OTHER INFORMATION: Xaa is Ala or Val

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

25

Xaa Xaa Tyr Ile Pro Xaa Xaa Gly Xaa Pro Xaa Gly Gly Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 64:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Val or Leu

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: Xaa is Ala or Gly

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Tyr Ile Pro Xaa Xaa Gly Xaa Pro Xaa  
1 5

10

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 25 (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- 30 (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Val or Leu

(ix) FEATURE:

- 35 (A) NAME/KEY: misc-feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: Xaa is Ala or Gly

40 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Ile Pro Xaa Xaa Gly Xaa Pro Xaa  
1 5

50

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 1

(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 2

(D) OTHER INFORMATION: Xaa is Val or Leu

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 4

(D) OTHER INFORMATION: Xaa is Ala or Gly

20

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 6

(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

25

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 9

(D) OTHER INFORMATION: Xaa is Ala or Val

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Xaa Xaa Gly Xaa Pro Xaa Gly Gly Xaa  
1 5

40

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS;

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala  
1 5 10 15

55

Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr  
20 25 30

5 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
35 40

(2) INFORMATION FOR SEQ ID NO: 68:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 20 (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Val or Leu

25 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Ala or Gly

30 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 5  
35 (D) OTHER INFORMATION: Xaa is Leu or Val or lie

(ix) FEATURE:

- 40 (A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Ala or Val

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

45 Xaa Gly Xaa Pro Xaa Gly Gly Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 69:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
55 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

EP 0 725 824 B1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

5                                   Leu Met Gly Tyr Ile Pro Leu Val  
                                  1                                   5

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS;

- 10                   (A) LENGTH: 7 amino acids  
                  (B) TYPE: amino acid  
                  (C) STRANDEDNESS: single  
                  (D) TOPOLOGY: linear

15                   (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

20                                   Met Gly Tyr Ile Pro Leu Val  
                                  1                                   5

(2) INFORMATION FOR SEQ ID NO: 71:

25                   (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
                  (B) TYPE: amino acid  
30                   (C) STRANDEDNESS: single  
                  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

                                  Tyr Ile Pro Leu Val Gly Ala Pro Leu  
                                  1                                   5

40                   (2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- 45                   (A) LENGTH: 8 amino acids  
                  (B) TYPE: amino acid  
                  (C) STRANDEDNESS: single  
                  (D) TOPOLOGY: linear

50                   (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

55                                   Ile Pro Leu Val Gly Ala Pro Leu  
                                  1                                   5

(2) INFORMATION FOR SEQ ID NO: 73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Val Leu Glu Asp Ile Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys  
 1 5 10 15  
 Ser Phe Ser Ile  
 20

## (2) INFORMATION FOR SEQ ID NO: 74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: Xaa is Val or Ile

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: Xaa is Phe or Tyr

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: Xaa is Ala or Pro

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: Xaa is Leu or Ile

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Gly Xaa Asn Xaa Xaa Thr Gly Asn Xaa  
 1 5

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 15 (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Val or Ile

(ix) FEATURE:

- 20 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Phe or Tyr

(ix) FEATURE:

- 25 (A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is Ala or Pro

(ix) FEATURE:

- 30 (A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Leu or Ile

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

40 Xaa Asn Xaa Xaa Thr Gly Asn Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 55 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Leu or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Asn Xaa Pro Gly Cys Ser Phe Ser Ile  
1 5

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) **FEATURE:**

20 (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Leu or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Xaa Pro Gly Cys Ser Phe Ser Ile  
1 5

30 (2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

45 Gly Val Asn Tyr Ala Thr Gly Asn Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Gly Val Asn Tyr Ala Thr Gly Asn Leu  
1 5

5 (2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Asn Leu Pro Gly Cys Ser Phe Ser Ile  
1 5

20

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

35

Leu Pro Gly Cys Ser Phe Ser Ile  
1 5

(2) INFORMATION FOR SEQ ID NO: 82:

40

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Ala or Thr or Glu

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature

(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Ala or Glu

(ix) FEATURE:

5

(A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Val or Ala or Leu

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 9  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

20

Xaa Leu Xaa His Gly Val Arg Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

35

(A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Ala or Glu

(ix) FEATURE:

40

(A) NAME/KEY: misc-feature  
(B) LOCATION: 7  
(D) OTHER INFORMATION: Xaa is Val or Ala or Leu

45

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Leu or Val or Ile

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

55

Leu Xaa His Gly Val Arg Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 84:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Val or Ala or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: Xaa is Glu or Gly

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: Xaa is Val or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly Val Arg Xaa Xaa Xaa Asp Gly Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Val or Ala or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Glu or Gly

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: Xaa is Val or Ile

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

20

Val Arg Xaa Xaa Xaa Asp Gly Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 86:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

35

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Val or Ala or Leu

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Glu or Gly

50

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: Xaa is Val or Ile

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: Xaa is Phe or Tyr

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

**Arg Xaa Xaa Xaa Asp Gly Xaa Asn Xaa**  
**1 5**

10

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 25 (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Val or Ala or Leu

(ix) FEATURE:

- 30 (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Leu or Val or Ile

(ix) FEATURE:

- 35 (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Glu or Gly

40 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: Xaa is Val or Ile

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 8
- 50 (D) OTHER INFORMATION: Xaa is Phe or Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

55 **Xaa Xaa Xaa Asp Gly Xaa Asn Xaa**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS;

- (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ala Leu Ala His Gly Val Arg Val Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Leu Ala His Gly Val Arg Val Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Val Arg Val Leu Glu Asp Gly Val  
1 5

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

5

Arg Val Leu Glu Asp Gly Val  
1 5

(2) INFORMATION FOR SEQ ID NO: 92:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Val Leu Glu Asp Gly Val Asn Tyr  
1 5

25

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Leu Glu Asp Gly Val Asn Tyr  
1 5

40

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

55

Leu Val Gly Ala Pro Leu Gly Gly Ala  
1 5

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

15 Val Gly Ala Pro Leu Gly Gly Ala  
1 5

(2) INFORMATION FOR SEQ ID NO: 96:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 30 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Leu or Val or Phe

35 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is Lys or Arg

40 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 9  
45 (D) OTHER INFORMATION: Xaa is Leu or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

50 Asn Xaa Gly Xaa Val Ile Asp Thr Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 97:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Leu or Val or Phe

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Lys or Arg

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Leu or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Xaa Gly Xaa Val Ile Asp Thr Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Asn Leu Gly Lys Val Ile Asp Thr Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

EP 0 725 824 B1

(A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Arg or Lys

5 (ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Ala or Ser or Thr

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 5  
(D) OTHER INFORMATION: Xaa is Ala or Gly

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: Xaa is Gin or Lys or Arg

20

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 9  
(D) OTHER INFORMATION: Xaa is Tyr or His

25

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Gly or Ala

30

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 17  
(D) OTHER INFORMATION: Xaa is Glu or Lys

35

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 19  
(D) OTHER INFORMATION: Xaa is Cys or Met or Leu

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

50

Gly Xaa Xaa Trp Xaa Xaa Pro Gly Xaa Pro Trp Pro Leu Tyr Xaa Asn  
1 5 10 15  
Xaa Gly Xaa Gly  
20

55

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDBDNNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Ala or Ser or Thr

(ix) FEATURE:

15

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Ala or Gly

20

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Gln or Lys or Arg

25

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: Xaa is Tyr or His

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

35

Xaa Trp Xaa Xaa Pro Gly Xaa Pro Trp  
1 5

(2) INFORMATION FOR SEQ ID NO: 101:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

50

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Ala or Gly

55

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3

(D) OTHER INFORMATION: Xaa is Gln or Lys or Arg

(ix) FEATURE:

- 5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: Xaa is Tyr or His

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

10

Trp Xaa Xaa Pro Gly Xaa Pro Trp  
1 5

15 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

30 Thr Trp Ala Gln Pro Gly Tyr Pro Trp  
1 5

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

45 Trp Ala Gln Pro Gly Tyr Pro Trp  
1 5

(2) INFORMATION FOR SEQ ID NO: 104:

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

**EP 0 725 824 B1**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

[illegible]

30 (2) INFORMATION FOR SEO ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

45 Thr Pro Thr Val Ala Thr Thr Arg Asp Gly Lys Leu Pro Ala Thr Gln  
1 5 10 15  
Leu Arg

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

5      Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
       1                      5                      10                      15  
       Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val  
                     20                      25                      30  
 10      Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys  
                     35                      40                      45  
       Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp  
                     50                      55                      60  
 15      Asp Met Met Met Asn Trp Ser Pro Thr Ala Ala Leu  
                     65                      70                      75

## (2) INFORMATION FOR SEQ ID NO: 107:

## 20      (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 25      (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## 30      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Met Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg  
       1                      5                      10                      15  
 35      Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val  
                     20                      25                      30  
       Leu Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Met Ala Lys Val  
                     35                      40                      45  
 40      Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val  
                     50                      55                      60  
       Ser Gly Gly Gln Ala  
       65

## 45      (2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids  
 50      (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

55

## (ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Gly or Arg

(ix) FEATURE:

5

(A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Gly or Ala or Lys

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is Ala or Val or Gly or Ser or Asp

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 5  
(D) OTHER INFORMATION: Xaa is Gly or Phe or Tyr

20

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 7  
(D) OTHER INFORMATION: Xaa is Asn or His or Arg or Leu or Ala or Ser

25

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Thr or Ser

30

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 9  
(D) OTHER INFORMATION: Xaa is Met or Ile

35

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 10  
(D) OTHER INFORMATION: Xaa is Asp

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 12  
(D) OTHER INFORMATION: Xaa is His or Leu or Val or Thr or Ile

45

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 21  
(D) OTHER INFORMATION: Xaa is His or Tyr

55

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 23  
(D) OTHER INFORMATION: Xaa is Asp or Glu

5 (ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 24  
(D) OTHER INFORMATION: Xaa is Ala or Thr

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 27  
(D) OTHER INFORMATION: Xaa is Ser or Thr or Ile or Leu

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 28  
(D) OTHER INFORMATION: Xaa is Arg or Lys

20

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 31  
(D) OTHER INFORMATION: Xaa is Ser or Ala

25

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 34  
(D) OTHER INFORMATION: Xaa is Trp or Leu

30

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 35  
(D) OTHER INFORMATION: Xaa is Ile or Leu

35

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 40  
(D) OTHER INFORMATION: Xaa is Leu or Met or Ile

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 41  
(D) OTHER INFORMATION: Xaa is Val or Ile

50

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 54  
(D) OTHER INFORMATION: Xaa is Ile or Val or Phe or Leu

55

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 56  
 (D) OTHER INFORMATION: Xaa is Tyr or Phe

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 57  
 (D) OTHER INFORMATION: Xaa is Thr or Ser or Ala

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 58  
 (D) OTHER INFORMATION: Xaa is Ile or Val

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 61  
 (D) OTHER INFORMATION: Xaa is Ile or Val or Ala

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 64  
 (D) OTHER INFORMATION: Xaa is Tyr or Phe

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

Ile Xaa Xaa Xaa Xaa Asn Xaa Xaa Glx Glx Leu Xaa Cys Pro Thr Asp
1      5      10      15
Cys Phe Arg Lys Xaa Pro Xaa Xaa Thr Tyr Xaa Xaa Cys Gly Xaa Gly
20      25      30
Pro Xaa Xaa Thr Pro Arg Cys Xaa Xaa Asp Tyr Pro Tyr Arg Leu Trp
35      40      45
His Tyr Pro Cys Thr Xaa Asn Xaa Xaa Xaa Phe Lys Xaa Arg Met Xaa
50      55      60
Val Gly Gly Val Glu His
65      70

```

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Gln or Ser or Tyr

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Xaa is Ile or Val

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: Xaa is Thr or Ser

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

20

**Xaa Leu Xaa Asn Xaa Asn Gly Ser Trp**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 110:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

35

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Ile or Val

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Xaa is Thr or Ser

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

50

**Leu Xaa Asn Xaa Asn Gly Ser Trp**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 4

(D) OTHER INFORMATION: Xaa is Leu or Ile

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 6

(D) OTHER INFORMATION: Xaa is Ser or Arg

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

20

Ser Trp His Xaa Asn Xaa Thr Ala Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 112:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

35

(A) NAME/KEY: misc-feature

(B) LOCATION: 4

(D) OTHER INFORMATION: Xaa is Leu or Ile

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 6

(D) OTHER INFORMATION: Xaa is Ser or Arg

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

50

Ser Trp His Xaa Asn Xaa Thr Ala Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 113:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Gln Leu Ile Asn Thr Asn Gly Ser Trp  
1 5

10

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

25

Leu Ile Asn Thr Asn Gly Ser Trp  
1 5

(2) INFORMATION FOR SEQ ID NO: 115:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

40

Ser Trp His Ile Asn Ser Thr Ala Leu  
1 5

45

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Trp His Ile Asn Ser Thr Ala Leu  
1 5

5 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Trp His Ile Asn Ser Thr Ala Leu  
1 5

20

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Gly Gly Val Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu  
1 5 10 15  
Asp Gly Val Asn Tyr  
20

40

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 55 (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Thr or Ser

(ix) FEATURE:

EP 0 725 824 B1

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Met or Ile

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Asp

10

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 5  
(D) OTHER INFORMATION: Xaa is His or Leu or Val or Thr or Ile

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

20

Xaa Glx Glx Leu Xaa Cys Pro Thr Asp Cys Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 120:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

35

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is His or Tyr

40

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: Xaa is Asp or Glu

45

(ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 7  
(D) OTHER INFORMATION: Xaa is Ala or Thr

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

55

Phe Arg Lys Xaa Pro Xaa Xaa Thr Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Trp or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Ile or Leu

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: Xaa is Leu or Met or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: Xaa is Val or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

**Xaa Xaa Thr Pro Arg Cys Xaa Xaa**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Leu or Met or Ile

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Xaa is Val or Ile

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Xaa Xaa Asp Tyr Pro Tyr Arg Leu  
1 5

10

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Xaa is Val or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

30

Xaa Asp Tyr Pro Tyr Arg Leu Trp  
1 5

(2) INFORMATION FOR SEQ ID NO: 124:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Pro Tyr Arg Leu Trp His Tyr  
1 5

50

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Ile or Val or Phe or Leu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

10

Leu Trp His Tyr Pro Cys Thr Xaa  
1 5

15 (2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25

(ix) FEATURE:

- 30 (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Ile or Val or Phe or Leu

(ix) FEATURE:

- 35 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Tyr or Phe

(ix) FEATURE:

- 40 (A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is Thr or Ser or Ala

(ix) FEATURE:

45

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 5  
(D) OTHER INFORMATION: Xaa is Ile or Val

(ix) FEATURE:

50

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 8  
(D) OTHER INFORMATION: Xaa is Ile or Val or Ala

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Xaa Asn Xaa Xaa Xaa Phe Lys Xaa  
1 5

5 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(ix) FEATURE:

- 20 (A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Tyr or Phe

(ix) FEATURE:

- 25 (A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Thr or Ser or Ala

(ix) FEATURE:

- 30 (A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
(D) OTHER INFORMATION: Xaa is Ile or Val

(ix) FEATURE:

- 35 (A) NAME/KEY: misc-feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: Xaa is Ile or Val or Ala

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Xaa Xaa Xaa Phe Lys Xaa Arg Met  
1 5

45

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 8 amino acids.  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:



(A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Ile or Val

5 (ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is Ile or Val or Ala

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 7  
(D) OTHER INFORMATION: Xaa is Tyr or Phe

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

20

**Xaa Phe Lys Xaa Arg Met Xaa Val**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 129:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

35

(A) NAME/KEY: misc-feature  
(B) LOCATION: 1  
(D) OTHER INFORMATION: Xaa is Ile or Val or Ala

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: Xaa is Tyr or Phe

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

50

**Xaa Arg Met Xaa Val Gly Gly Val**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 130:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 2

(D) OTHER INFORMATION: Xaa is Gly or Arg

10

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 3

(D) OTHER INFORMATION: Xaa is Gly or Ala or Lys

15

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 4

(D) OTHER INFORMATION: Xaa is Ala or Val or Gly or Ser or Asp

20

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 5

(D) OTHER INFORMATION: Xaa is Gly or Phe or Tyr

25

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 7

(D) OTHER INFORMATION: Xaa is Asn or His or Arg or Leu or Ala or Ser

30

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 8

(D) OTHER INFORMATION: Xaa is Thr or Ser

35

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 9

(D) OTHER INFORMATION: Xaa is Met or Ile

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 10

(D) OTHER INFORMATION: Xaa is Asp

50

(ix) FEATURE:

(A) NAME/KEY: misc-feature

(B) LOCATION: 12

(D) OTHER INFORMATION: Xaa is His or Leu or Val or Thr or Ile

55

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: Xaa is His or Tyr

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Ile Xaa Xaa Xaa Xaa Asn Xaa Xaa Glx Glx Leu Xaa Cys Pro Thr Asp  
 1 5 10 15  
 Cys Phe Arg Lys Xaa Pro  
 20

## (2) INFORMATION FOR SEQ ID NO: 131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: Xaa is His or Tyr

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: Xaa is Asp or Glu

## (ix) FEATURE:

- (A) NAME/KEY: tnisc-feature  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: Xaa is Ala or Thr

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: Xaa is Ser or Thr or Ile or Leu

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 14  
 (D) OTHER INFORMATION: Xaa is Arg or Lys

## (ix) FEATURE:

1

(D) OTHER INFORMATION: Xaa is Ile or Leu

(ix) FEATURE:

5 (A) NAME/KEY: misc-feature  
(B) LOCATION: 14  
(D) OTHER INFORMATION: Xaa is Leu or Met or Ile

(ix) FEATURE:

10 (A) NAME/KEY: misc-feature  
(B) LOCATION: 15  
(D) OTHER INFORMATION: Xaa is Val or Ile

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Xaa Xaa Cys Gly Xaa Gly Pro Xaa Xaa Thr Pro Arg Cys Xaa Xaa Asp  
1 5 10 15  
Tyr Pro Tyr Arg  
20

(2) INFORMATION FOR SEQ ID NO: 133:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: Xaa is Leu or Met or Ile

40

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 3  
45 (D) OTHER INFORMATION: Xaa is Val or Ile

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 16  
50 (D) OTHER INFORMATION: Xaa is Ile or Val or Phe or Leu

(ix) FEATURE:

(A) NAME/KEY: misc-feature  
(B) LOCATION: 18  
55 (D) OTHER INFORMATION: Xaa is Tyr or Phe

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 19  
 (D) OTHER INFORMATION: Xaa is Thr or Ser or Ala

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: Xaa is Ile or Val

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Cys Xaa Xaa Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Xaa  
 1 5 10 15  
 Asn Xaa Xaa Xaa  
 20

## (2) INFORMATION FOR SEQ ID NO: 134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: Xaa is Ile or Val or Phe or Leu

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: Xaa is Tyr or Phe

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: Xaa is Thr or Ser or Ala

## (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: Xaa is Ile or Val

## (ix) FEATURE:

EP 0 725 824 B1

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 11  
(D) OTHER INFORMATION: Xaa is Ile or Val or Ala

5 (ix) FEATURE:

- (A) NAME/KEY: misc-feature  
(B) LOCATION: 14  
(D) OTHER INFORMATION: Xaa is Tyr or Phe

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

15 **Pro Cys Thr Xaa Asn Xaa Xaa Xaa Phe Lys Xaa Arg Met Xaa Val Gly**  
**1 5 10 15**  
**Gly Val Glu His**  
**20**

20 (2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

35 **Val Ala Lys Ala Val Asp Phe Val**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 136:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

50

**Val Ala Lys Ala Val Asp Phe Ile**  
**1 5**

(2) INFORMATION FOR SEQ ID NO: 137:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

10 Val Glu Ser Met Glu Thr Thr Met  
1 5

(2) INFORMATION FOR SEQ ID NO: 138:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

25

Ala Val Pro Gln Thr Phe Gln Val  
1 5

30 (2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

45 Tyr Ala Ala Gln Gly Tyr Lys Val  
1 5

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:



Val Leu Val Leu Asn Pro Ser Val Ala  
1 5

5 (2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Tyr Met Ser Lys Ala His Gly Val  
1 5

20

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Ile Arg Thr Gly Val Arg Thr Ile  
1 5

35

(2) INFORMATION FOR SEQ ID NO: 143:

40

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Tyr Ser Thr Tyr Gly Lys Phe Leu  
1 5

55

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

10

Ile Leu Gly Ile Gly Thr Val Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 145:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

Val Thr Val Pro His Pro Asn Ile  
1 5

30

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Ile Pro Phe Tyr Gly Lys Ala Ile  
1 5

45

(2) INFORMATION FOR SEQ ID NO: 147:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5 Phe Tyr Gly Lys Ala Ile Pro Ile  
1 5

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

20

Val Ile Lys Gly Gly Arg His Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 149:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

35

Ile Lys Gly Gly Arg His Leu Ile  
1 5

40

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

55

Phe Cys His Ser Lys Lys Lys Cys  
1 5

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Cys Asp Glu Leu Ala Ala Lys Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Leu Ala Ala Lys Leu Ser Gly Phe Gly  
 1 5

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Ser Gly Phe Gly Ile Asn Ala Val  
 1 5

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

5

Phe Gly Ile Asn Ala Val Ala Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO: 155:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Tyr Arg Gly Leu Asp Val Ser Val  
1 5

25

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Val Ile Pro Thr Ser Gly Asp Val  
1 5

40

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

50

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

55

Ile Pro Thr Ser Gly Asp Val Val  
1 5

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

15 Val Val Val Ala Thr Asp Ala Leu  
1 5

(2) INFORMATION FOR SEQ ID-NO: 159:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

30 Val Val Ala Thr Asp Ala Leu Met  
1 5

35 (2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
40 (B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

50 Met Thr Gly Phe Thr Gly Asp Phe  
1 5

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Phe Thr Gly Asp Phe Asp Ser Val  
1 5

10

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

25 Val Ile Asp Cys Asn Thr Cys Val  
1 5

(2) INFORMATION FOR SEQ ID NO: 163:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Ala Leu Met Gly Tyr Ile Pro Leu Val  
1 5

45 (2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys  
1 5 10 15

Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile Leu His Thr  
20 25 30

Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn  
35 40

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro  
1 5 10 15

Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile Leu His Thr Pro  
20 25 30

Gly Cys Val Pro Cys Val Arg Glu Gly Asn  
35 40

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: -linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Lys Leu Val Ala Leu Gly Ile Asn Ala Val  
1 5 10

## Claims

1. Use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 157 to 176 of the core region of HCV:

NH<sub>2</sub>X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGNX<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 51), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 13, and wherein X<sub>30</sub> represents V or A or L, X<sub>31</sub>



represents L or V or I,  $X_{32}$  represents E or G,  $X_{33}$  represents V or I, and  $X_{34}$  represents F or Y,  $X_{35}$  represents A or P,  $X_{36}$  represents L or I.

2. Use according to claim 1, for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 157 to 176 of the core region of HCV:

**VLEDGVNYATGNLPGCSFSI (SEQ ID NO 13 = peptide CORE 27) or**  
**VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73).**

3. Use according to claim 1, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

**$\text{NH}_2\text{-GX}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 74),**  
 **$\text{NH}_2\text{-X}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 75),**  
 **$\text{NH}_2\text{-NX}_{36}\text{PGCSFSI-COOH}$  (SEQ ID NO 76) and**  
 **$\text{NH}_2\text{-X}_{36}\text{PGCSFSI-COOH}$  (SEQ ID NO 77).**

4. Use according to claim 1, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

**GVNYATGNL (SEQ ID NO 78),**  
**NLPGCSFSI (SEQ ID NO 80) and**  
**LPGCSFSI (SEQ ID NO 81).**

5. Use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 145 to 164 of the core region of HCV:  
 $\text{NH}_2\text{-GGX}_{25}\text{X}_{26}\text{X}_{27}\text{X}_{28}\text{LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 52), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 12, and wherein  $X_{25}$  represents A or V,  $X_{26}$  represents A or S,  $X_{27}$  represents R or A,  $X_{28}$  represents A or T or E,  $X_{29}$  represents A or E,  $X_{30}$  represents V or A or L,  $X_{31}$  represents L or V or I,  $X_{32}$  represents E or G,  $X_{33}$  represents V or I, and  $X_{34}$  represents F or Y.

6. Use according to claim 5, for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 145 to 164 of the core region of HCV:

**GGAARALAHGVRVLEDGVNY (SEQ ID NO 12 = peptide CORE 25) or**  
**GGVAARALAHGVRVLEDGVNY (SEQ ID NO 118).**

7. Use according to claim 5, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

$\text{NH}_2\text{-X}_{28}\text{LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{-COOH}$  (SEQ ID NO 82),  
 $\text{NH}_2\text{-LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{-COOH}$  (SEQ ID NO 83),  
 $\text{NH}_2\text{-GVRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{-COOH}$  (SEQ ID NO 84),  
 $\text{NH}_2\text{-VRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{-COOH}$  (SEQ ID NO 85),  
 $\text{NH}_2\text{-RX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 86), and  
 $\text{NH}_2\text{-X}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 87).

8. Use according to claim 5, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

ALAHGVRVL (SEQ ID NO 88),  
 LAHGVRVL (SEQ ID NO 89),  
 VRVLEDGV (SEQ ID NO 90),

RVLEDGV (SEQ ID NO 91),  
 VLEDGVNY (SEQ ID NO 92), and  
 LEDGVNY (SEQ ID NO 93).

9. Use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 133 to 152 or the core region of HCV:

$\text{NH}_2\text{-LX}_{19}\text{X}_{20}\text{YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{X}_{26}\text{X}_{27}\text{X}_{28}\text{LX}_{29}\text{-COOH}$  (SEQ ID NO 53), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 11, and wherein  $\text{X}_{19}$  represents M or I,  $\text{X}_{20}$  represents G or E,  $\text{X}_{21}$  represents L or V or I,  $\text{X}_{22}$  represents V or L,  $\text{X}_{23}$  represents A or G,  $\text{X}_{24}$  represents L, V or I,  $\text{X}_{25}$  represents A or V,  $\text{X}_{26}$  represents A or S,  $\text{X}_{27}$  represents R or A,  $\text{X}_{28}$  represents A or T or E,  $\text{X}_{29}$  represents A or E.

10. Use according to claim 9, for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 133 to 152 of the core region of HCV: LMGYIPLVGAPLGAARALA (SEQ ID NO 11 = peptide CORE 23).

11. Use according to claim 9, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following list of peptides:

$\text{NH}_2\text{-LX}_{19}\text{X}_{20}\text{YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}$  (SEQ ID NO 62),  
 $\text{NH}_2\text{[-X}_{19}\text{X}_{20}\text{YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}]$  (SEQ ID NO 63),  
 $\text{NH}_2\text{-YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{-COOH}$  (SEQ ID NO 64),  
 $\text{NH}_2\text{-IPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{-COOH}$  (SEQ ID NO 65),  
 $\text{NH}_2\text{-X}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}$  (SEQ ID NO 66) [-], and  
 $\text{NH}_2\text{-X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}$  (SEQ ID NO 68).

12. Use according to claim 9, for the preparation of an HCV immunogenic composition, with said polypeptide being

chosen from the following list of peptides:

LMGYIPLV (SEQ ID NO 69),

MGYIPLV (SEQ ID NO 70),

YIPLVGAPL (SEQ ID NO 71),

IPLVGAPL (SEQ ID NO 72),

LVGAPLGGA (SEQ ID NO 94), and

VGAPLGGA (SEQ ID NO 95).

13. Use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 109 to 128 of the core region of HCV:

NH<sub>2</sub>-X<sub>11</sub>X<sub>12</sub>DPRX<sub>13</sub>X<sub>14</sub>SRNX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>TC-COOH (SEQ ID NO 54), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 9, and wherein X<sub>11</sub> represents P or Q, X<sub>12</sub> represents N or T, X<sub>13</sub> represents R or H, X<sub>14</sub> represents R or K, X<sub>15</sub> represents L or V or F, X<sub>16</sub> represents K or R, X<sub>17</sub> represents L or I.

14. Use according to claim 13, for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of about 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 109 to 128 of the core region of HCV: PTDPRRRSRNLGKVIDTLTC (SEQ ID NO 9 = peptide CORE 19).

15. Use according to claim 13, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following peptides:

NH<sub>2</sub>-NX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 96), and

NH<sub>2</sub>-X<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 97).

16. Use according to claim 13, for the preparation of an HCV immunogenic composition, with said polypeptide being chosen from the following peptides:

NLGKVIDTL (SEQ ID NO 98), and

LGKVIDTL (SEQ ID NO 117).

17. Use of a polypeptide of about 8 to about 20 amino acids for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of at least 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 73 to 92 of the core region of HCV:

NH<sub>2</sub>-GX<sub>1</sub>X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PWPLYX<sub>6</sub>NX<sub>7</sub>GX<sub>8</sub>G-COOH (SEQ ID NO 99), and with said contiguous amino acids containing a T-cell stimulating epitope, and wherein said polypeptide mimics the T-cell immunological stimulation properties of the polypeptide as represented in SEQ ID NO 6, and wherein X<sub>1</sub> represents R or K, X<sub>2</sub> represents A, S or T, X<sub>3</sub> represents A or G, X<sub>4</sub> represents Q, K or R, X<sub>5</sub> represents Y or H, X<sub>6</sub> represents G or A, X<sub>7</sub> represents E or K, and X<sub>8</sub> represents C, M or L.

18. Use according to claim 17, for the preparation of an HCV immunogenic composition, with said polypeptide comprising or consisting of a least 8 to about 20 contiguous amino acids selected from the region comprised between amino acid positions 73 to 92 of the core region of HCV:

**GRTWAQPGYPWPLYGNEGCG (SEQ ID NO 6 = peptide CORE 13).**

- 5 19. Use according to claim 17, for the preparation of an HCV immunogenic composition, with said polypeptide being selected from:

**NH<sub>2</sub>-X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 100) and**

10 **NH<sub>2</sub>-WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 101).**

20. Use according to claim 17, for the preparation of an HCV immunogenic composition, with said polypeptide being selected from:

15 **TWAQPGYPW (SEQ ID NO 102), and**

**WAQPGYPW (SEQ ID NO 103).**

- 20 21. Use according to any of claims 1 to 20, wherein said T-cell stimulating epitope is a T-cell helper epitope.

22. Use according to any of claims 1 to 20, wherein said T-cell stimulating epitope is a CTL epitope.

- 25 23. Use according to any of claims 1 to 22, wherein said polypeptide is incorporated into a prophylactic vaccine composition.

24. Use according to any of claims 1 to 22, wherein said polypeptide is incorporated into a therapeutic vaccine composition.

- 30 25. A polypeptide consisting of multiple repeats, combinations or mimotopes of any of the contiguous amino acid sequences selected to contain a T-cell stimulating epitope[s] as defined in any of claims 1 to 22, with said combinations comprising two or more peptides joined into a single structure and with said mimotopes having one or more amino acid variations compared to said peptides as long as said mimotope peptides are capable of providing for immunological stimulation after which the T-cells are reactive with at least one strain of HCV.

- 35 26. Use according to any of claims 1 to 24, with said polypeptide being a recombinant polypeptide expressed by means of an expression vector comprising a nucleic acid insert encoding a polypeptide according to any of claims 1 to 22.

- 40 27. Use according to any of claims 1 to 24, wherein said polypeptide is operably linked to a pathogen related immunogen, such as the HCV envelope proteins E1 and E2, or the HCV NS3, NS4 or NS5 immunogens, or a HCV peptide containing a B cell stimulating epitope.

- 45 28. A peptide consisting of at least 8 contiguous amino acids of the sequence of any of the following peptides, with said peptides containing a T-cell epitope:

a)

NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 51)  
VLEDGVNYATGNLPGCSFSI (SEQ ID NO 13 = peptide CORE 27),  
VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73),  
NH<sub>2</sub>-GX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>-COOH (SEQ ID NO 74),  
NH<sub>2</sub>-X<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>-COOH (SEQ ID NO 75),  
NH<sub>2</sub>-NX<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 76),

NH<sub>2</sub>-X<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 77),  
GVNYATGNL (SEQ ID NO 78), [or]  
NLPGCSFSI (SEQ ID NO 80), or  
LPGCSFSI (SEQ ID NO 81),

wherein said peptide mimics the T-cell immunological stimulation properties of the peptide represented in SEQ ID NO 13;

b)

NH<sub>2</sub>-GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 52),  
GGAARALAHGVRVLEDGVNY (SEQ ID NO 12 = peptide CORE 25),  
GGVAARALAHGVRVLEDGVNY (SEQ ID NO 118),  
NH<sub>2</sub>-X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 82),  
NH<sub>2</sub>-LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 83),  
NH<sub>2</sub>-GVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 84),  
NH<sub>2</sub>-VRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 85),  
NH<sub>2</sub>-RX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 86),  
NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 87),  
ALAHGVRVL (SEQ ID NO 88),  
LAHGVRVL (SEQ ID NO 89),  
VRVLEDGV (SEQ ID NO 90),  
RVLEDGV (SEQ ID NO 91),  
VLEDGVNY (SEQ ID NO 92), or  
LEDGVNY (SEQ ID NO 93),

wherein said peptide mimics the T-cell immunological stimulation properties of the peptide represented in SEQ ID NO 12;

c)

NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>-COOH (SEQ ID NO 53),  
 5 LMGYIPLVGAPLGGAARALA (SEQ ID NO 11 = peptide CORE 23),  
 NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 62),  
 NH<sub>2</sub>-X<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 63),  
 10 NH<sub>2</sub>-YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 64),  
 NH<sub>2</sub>-IPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 65),  
 NH<sub>2</sub>-X<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 66),

15  
 NH<sub>2</sub>-X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 68),  
 LMGYIPLV (SEQ ID NO 69),  
 20 MGYIPLV (SEQ ID NO 70),  
 YIPLVGAPL (SEQ ID NO 71),  
 IPLVGAPL (SEQ ID NO 72), [er]  
 25 LVGAPLGGA (SEQ ID NO 94), or  
 VGAPLGGA (SEQ ID NO 95),

30 wherein said peptide mimics the T-cell immunological stimulation properties of the peptide represented in SEQ ID NO 11;

d)

35 NH<sub>2</sub>-X<sub>11</sub>X<sub>12</sub>DPRX<sub>13</sub>X<sub>14</sub>SRNX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>TC -COOH (SEQ ID NO 54),  
 PTDPRRRSRNLGKVIDTLTC (SEQ ID NO 9 = peptide CORE 19),  
 40 NH<sub>2</sub>-NX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 96),  
 NH<sub>2</sub>-X<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 97), [er]  
 NLGKVIDTL (SEQ ID NO 98), or  
 45 LGKVIDTL (SEQ ID NO 117),

50 wherein said peptide mimics the T-cell immunological stimulation properties of the peptide as represented in SEQ ID NO 9;

e)

NH<sub>2</sub>-GX<sub>1</sub>X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PWPLYX<sub>6</sub>NX<sub>7</sub>GX<sub>8</sub>G-COOH (SEQ ID NO 99),  
 GRTWAQPGYPWPLYGNEGCG (SEQ ID NO 6 = peptide CORE 13),  
 NH<sub>2</sub>-X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 100),  
 NH<sub>2</sub>-WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 101), [or]  
 TWAQPGYPW (SEQ ID NO 102), or  
 WAQPGYPW (SEQ ID NO 103),

wherein said peptide mimics the T-cell immunological stimulation properties of the peptide as represented in SEQ ID NO 6;

wherein X<sub>1</sub> represents R or K, X<sub>2</sub> represents A, S or T, X<sub>3</sub> represents A or G, X<sub>4</sub> represents Q, K or R, X<sub>5</sub> represents Y or H, X<sub>6</sub> represents G or A, X<sub>7</sub> represents E or K, X<sub>8</sub> represents C, M or L, X<sub>9</sub> represents W or L, X<sub>10</sub> represents S, N, T, D or H, X<sub>11</sub> represents P or Q, X<sub>12</sub> represents N or T, X<sub>13</sub> represents R or H, X<sub>14</sub> represents R or K, X<sub>15</sub> represents L or V or F, X<sub>16</sub> represents K or R, X<sub>17</sub> represents L or I, X<sub>18</sub> represents F or L, X<sub>19</sub> represents M or I, X<sub>20</sub> represents G or E, X<sub>21</sub> represents L or V or I, X<sub>22</sub> represents V or L, X<sub>23</sub> represents A or G, X<sub>24</sub> represents L, V or I, X<sub>25</sub> represents A or V, X<sub>26</sub> represents A or S, X<sub>27</sub> represents R or A, X<sub>28</sub> represents A or T or E, X<sub>29</sub> represents A or E, X<sub>30</sub> represents V or A or L, X<sub>31</sub> represents L or V or I, X<sub>32</sub> represents E or G, X<sub>33</sub> represents V or I, X<sub>34</sub> represents F or Y, X<sub>35</sub> represents A or P, and X<sub>36</sub> represents L or I.

29. An immunogenic composition consisting of or comprising at least one of the peptides or polypeptides according to claim 28 mixed with a pharmaceutically acceptable excipient.

30. A vaccine composition according to claim 29.

31. A prophylactic vaccine composition according to claim 30.

32. A therapeutic vaccine composition according to claim 30.

33. A composition according to any of claims 29 to 32, with said composition comprising in addition to any of the polypeptides according to claim 28, a peptide or polypeptide containing at least one B cell stimulating epitope of HCV, and/or a structural HCV polypeptide, and/or a non-structural HCV polypeptide.

34. A composition according to any of claims 29 to 33, wherein said polypeptide according to claim 28 is mixed with HBsAg or HBcAg particles, HBV immunogens, HIV immunogens and/or HTLV immunogens.

35. Use of a recombinant expression vector comprising a nucleic acid insert encoding a polypeptide as defined in any of claims 1 to 22[24] for the preparation of a HCV immunogenic composition.

#### Patentansprüche

1. Verwendung eines Polypeptids aus etwa 8 bis etwa 20 Aminosäuren zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 157 bis 176 des HCV-Kernbereichs umfaßten Bereich:

NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGNX<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 51), umfaßt bzw. aus diesen besteht und wobei die aufeinanderfolgenden Aminosäuren ein T-Zellen stimulierendes Epitop enthalten, und worin das Polypeptid die Charakteristik des wie in SEQ ID NO 13 dargestellten Polypeptids, T-Zellen immunologisch zu stimulieren, imitiert, und worin X<sub>30</sub> für V oder A oder L, X<sub>31</sub> für L oder V oder I, X<sub>32</sub> für E oder G, X<sub>33</sub> für V oder I, X<sub>34</sub> für F oder Y, X<sub>35</sub> für A oder P und X<sub>36</sub> für L oder I steht.

2. Verwendung nach Anspruch 1 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 157 bis 176 des HCV-Kernbereichs umfaßten Bereich:

VLEDGVNYATGNLPGCSFSI (SEQ ID NO 13 = Peptid CORE 27) oder  
VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73), umfaßt bzw. aus diesen besteht.

3. Verwendung nach Anspruch 1 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von der folgenden Liste von Peptiden gewählt wird:

NH<sub>2</sub>-GX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGNX<sub>36</sub>-COOH (SEQ ID NO 74),  
NH<sub>2</sub>-X<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGNX<sub>36</sub>-COOH (SEQ ID NO 75),  
NH<sub>2</sub>-NX<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 76) und  
NH<sub>2</sub>-X<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 77).

4. Verwendung nach Anspruch 1 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von der folgenden Liste von Peptiden gewählt wird:

GVNYATGNL (SEQ ID NO 78),  
NLPGCSFSI (SEQ ID NO 80) und  
LPGCSFSI (SEQ ID NO 81).

5. Verwendung eines Polypeptids aus etwa 8 bis etwa 20 Aminosäuren zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 145 bis 164 des HCV-Kernbereichs umfaßten Bereich:

NH<sub>2</sub>-GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 52), umfaßt bzw. aus diesen besteht und wobei die aufeinanderfolgenden Aminosäuren ein T-Zellen stimulierendes Epitop enthalten, und worin das Polypeptid die Charakteristik des wie in SEQ ID NO 12 dargestellten Polypeptids, T-Zellen immunologisch zu stimulieren, imitiert, und worin X<sub>25</sub> für A oder V, X<sub>26</sub> für A oder S, X<sub>27</sub> für R oder A, X<sub>28</sub> für A oder T oder E, X<sub>29</sub> für A oder E, X<sub>30</sub> für V oder A oder L, X<sub>31</sub> für L oder V oder I, X<sub>32</sub> für E oder G, X<sub>33</sub> für V oder I und X<sub>34</sub> für F oder Y steht.

6. Verwendung nach Anspruch 5 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 145 bis 164 des HCV-Kernbereichs umfaßten Bereich:

GGAARALAHGVRVLEDGVNY (SEQ ID NO 12 = Peptid CORE 25) oder  
GGVAARALAHGVRVLEDGVNY (SEQ ID NO 118), umfaßt bzw. aus diesen besteht.

7. Verwendung nach Anspruch 5 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von der folgenden Liste von Peptiden gewählt wird:

NH<sub>2</sub>-X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 82),  
NH<sub>2</sub>-LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 83),  
NH<sub>2</sub>-GVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 84),  
NH<sub>2</sub>-VRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 85),  
NH<sub>2</sub>-RX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 86) und  
NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 87).

8. Verwendung nach Anspruch 5 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von der folgenden Liste von Peptiden gewählt wird:



ALAHGVRVL (SEQ ID NO 88),  
 LAHGVRVL (SEQ ID NO 89),  
 5 VRVLEDGV (SEQ ID NO 90),  
 RVLEDGV (SEQ ID NO 91),  
 VLEDGVNY (SEQ ID NO 92) und  
 10 LEDGVNY (SEQ ID NO 93).

9. Verwendung eines Polypeptids aus etwa 8 bis etwa 20 Aminosäuren zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 133 bis 152 des HCV-Kernbereichs umfaßten Bereich:

15 NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>-COOH (SEQ ID NO 53), umfaßt bzw. aus diesen besteht und wobei die aufeinanderfolgenden Aminosäuren ein T-Zellen stimulierendes Epitop enthalten, und worin das Polypeptid die Charakteristik des wie in SEQ ID NO 11 dargestellten Polypeptids, T-Zellen immunologisch zu stimulieren, imitiert, und worin X<sub>19</sub> für M oder I, X<sub>20</sub> für G oder E, X<sub>21</sub> für L oder V oder I, X<sub>22</sub> für V oder L, X<sub>23</sub> für A oder G, X<sub>24</sub> für L, V oder I, X<sub>25</sub> für A oder V, X<sub>26</sub> für A oder S, X<sub>27</sub> für R oder A, X<sub>28</sub> für A oder T oder E und X<sub>29</sub> für A oder E steht.

10. Verwendung nach Anspruch 9 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 133 bis 152 des HCV-Kernbereichs umfaßten Bereich:

25 LMGYIPLVGAPLGGAARALA (SEQ ID NO 11 = Peptid CORE 23), umfaßt bzw. aus diesen besteht.

11. Verwendung nach Anspruch 9 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von der folgenden Liste von Peptiden gewählt wird:

30 NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 62),  
 NH<sub>2</sub>-X<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 63),  
 NH<sub>2</sub>-YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 64),  
 35 NH<sub>2</sub>-IPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 65),  
 NH<sub>2</sub>-X<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 66) und  
 NH<sub>2</sub>-X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 68).

12. Verwendung nach Anspruch 9 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von der folgenden Liste von Peptiden gewählt wird:

45 LMGYIPLV (SEQ ID NO 69),  
 MGYIPLV (SEQ ID NO 70),  
 YIPLVGAPL (SEQ ID NO 71),  
 IPLVGAPL (SEQ ID NO 72),  
 50 LVGAPLGGA (SEQ ID NO 94) und  
 VGAPLGGA (SEQ ID NO 95).

13. Verwendung eines Polypeptids aus etwa 8 bis etwa 20 Aminosäuren zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 109 bis 128 des HCV-Kernbereichs umfaßten Bereich:

55 NH<sub>2</sub>-X<sub>11</sub>X<sub>12</sub>DPRX<sub>13</sub>X<sub>14</sub>SRNX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>TC-COOH (SEQ ID NO 54), umfaßt bzw. aus diesen besteht und

wobei die aufeinanderfolgenden Aminosäuren ein T-Zellen stimulierendes Epitop enthalten, und worin das Polypeptid die Charakteristik des wie in SEQ ID NO 9 dargestellten Polypeptids, T-Zellen immunologisch zu stimulieren, imitiert, und worin X<sub>11</sub> für P oder Q, X<sub>12</sub> für N oder T, X<sub>13</sub> für R oder H, X<sub>14</sub> für R oder K, X<sub>15</sub> für L oder V oder F, X<sub>16</sub> für K oder R und X<sub>17</sub> für L oder I steht.

14. Verwendung nach Anspruch 13 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid etwa 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 109 bis 128 des HCV-Kernbereichs umfaßten Bereich: PTDPRRRSRNLGKVIDTLTC (SEQ ID NO 9 = Peptid CORE 19), umfaßt bzw. aus diesen besteht.

15. Verwendung nach Anspruch 13 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von den folgenden Peptiden gewählt wird:

NH<sub>2</sub>-NX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 96) und  
NH<sub>2</sub>-X<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 97).

16. Verwendung nach Anspruch 13 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid von den folgenden Peptiden gewählt wird:

NLGKVIDTL (SEQ ID NO 98) und  
LGKVIDTL (SEQ ID NO 117).

17. Verwendung eines Polypeptids aus etwa 8 bis etwa 20 Aminosäuren zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid mindestens 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 73 bis 92 des HCV-Kernbereichs umfaßten Bereich:

NH<sub>2</sub>-GX<sub>1</sub>X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PWPLYX<sub>6</sub>NX<sub>7</sub>GX<sub>8</sub>-COOH (SEQ ID NO 99), umfaßt bzw. aus diesen besteht und wobei die aufeinanderfolgenden Aminosäuren ein T-Zellen stimulierendes Epitop enthalten, und worin das Polypeptid die Charakteristik des wie in SEQ ID NO 6 dargestellten Polypeptids, T-Zellen immunologisch zu stimulieren, imitiert, und worin X<sub>1</sub> für R oder K, X<sub>2</sub> für A, S oder T, X<sub>3</sub> für A oder G, X<sub>4</sub> für Q, K oder R, X<sub>5</sub> für Y oder H, X<sub>6</sub> für G oder A, X<sub>7</sub> für E oder K und X<sub>8</sub> für C, M oder L steht.

18. Verwendung nach Anspruch 17 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid mindestens 8 bis etwa 20 aufeinanderfolgende Aminosäuren, ausgewählt aus dem von den Aminosäurepositionen 73 bis 92 des HCV-Kernbereichs umfaßten Bereich:

GRTWAQPGYPWPLYGNEGCG (SEQ ID NO 6 = Peptid CORE 13),

umfaßt bzw. aus diesen besteht.

19. Verwendung nach Anspruch 17 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das Polypeptid ausgewählt wird aus:

NH<sub>2</sub>-X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 100) und  
NH<sub>2</sub>-WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 101).

20. Verwendung nach Anspruch 17 zur Herstellung einer HCV-immunogenen Zusammensetzung, wobei das

Polypeptid ausgewählt wird aus:

TWAQPGYPW (SEQ ID NO 102) und

WAQPGYPW (SEQ ID NO 103).

21. Verwendung nach einem der Ansprüche 1 bis 20, wobei es sich bei dem T-Zellen stimulierenden Epitop um ein T-Zellen-Helferepitop handelt.
22. Verwendung nach einem der Ansprüche 1 bis 20, wobei es sich bei dem T-Zellen stimulierenden Epitop um ein CTL-Epitop handelt.
23. Verwendung nach einem der Ansprüche 1 bis 22, wobei das Polypeptid in eine prophylaktische Impfstoffzusammensetzung integriert wird.
24. Verwendung nach einem der Ansprüche 1 bis 22, wobei das Polypeptid in eine therapeutische Impfstoffzusammensetzung integriert wird.
25. Polypeptid, bestehend aus mehrfachen Wiederholungen, Kombinationen oder Mimotopen einer beliebigen der aufgrund der in ihnen enthaltenen, eine T-Zelle stimulierenden Epitope gemäß einem der Ansprüche 1 bis 22 ausgewählten Sequenzen aus aufeinanderfolgenden Aminosäuren, wobei die Kombinationen zwei oder mehrere, zu einer einzigen Struktur verbundene Peptide umfassen und wobei die Mimotope verglichen mit den Peptiden eine oder mehrere Aminosäurevariationen aufweisen können, solange die mimotopischen Peptide in der Lage sind, für eine immunologische Stimulierung zu sorgen, wonach die T-Zellen auf wenigstens einen HCV-Stamm reagieren.
26. Verwendung nach einem der Ansprüche 1 bis 24, wobei es sich bei dem Polypeptid um ein rekombinantes Polypeptid handelt, das mittels eines für ein Polypeptid nach einem der Ansprüche 1 bis 22 codierende Nukleinsäureinsertion enthaltenden Expressionsvektors exprimiert wird.
27. Verwendung nach einem der Ansprüche 1 bis 24, wobei das Polypeptid mit einem mit einem Krankheitserreger in Zusammenhang stehenden Immunogen, wie z.B. den HCV-Hüllproteinen E1 und E2 oder den HCV-Immunogenen NS3, NS4 und NS5 oder einem ein B-Zellen stimulierendes Epitop enthaltenden HCV-Peptid, operativ verknüpft ist.
28. Peptid, bestehend aus mindestens 8 aufeinanderfolgenden Aminosäuren der Sequenz eines beliebigen der folgenden Peptide, wobei die Peptide ein T-Zellen-Epitop enthalten:

a)

$\text{NH}_2\text{-X}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{PGCSFSI-COOH}$  (SEQ ID NO 51),

VLEDGVNYATGNLPGCSFSI (SEQ ID NO 13 = Peptid CORE 27),

VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73),

$\text{NH}_2\text{-GX}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 74),

$\text{NH}_2\text{-X}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 75),

$\text{NH}_2\text{-NX}_{36}\text{PGCSFSI-COOH}$  (SEQ ID NO 76),

$\text{NH}_2\text{-X}_{36}\text{PGCSFSI-COOH}$  (SEQ ID NO 77),

GVNYATGNL (SEQ ID NO 78),

NLPGCSFSI (SEQ ID NO 80) oder

LPGCSFSI (SEQ ID NO 81),

worin das Peptid die Charakteristik des wie in SEQ ID NO 13 dargestellten Peptids, T-Zellen immunologisch zu stimulieren, imitiert;

b)

NH<sub>2</sub>-GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 52),

GGAARALAHGVRVLEDGVNY (SEQ ID NO 12 = Peptid CORE 25),

GGVAARALAHGVRVLEDGVNY (SEQ ID NO 118),

NH<sub>2</sub>-X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 82),

NH<sub>2</sub>-LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 83),

NH<sub>2</sub>-GVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 84),

NH<sub>2</sub>-VRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 85),

NH<sub>2</sub>-RX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 86),

NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 87),

ALAHGVRVL (SEQ ID NO 88),

LAHGVRVL (SEQ ID NO 89),

VRVLEDGV (SEQ ID NO 90),

RVLEDGV (SEQ ID NO 91),

VLEDGVNY (SEQ ID NO 92) oder

LEDGVNY (SEQ ID NO 93),

worin das Peptid die Charakteristik des wie in SEQ ID NO 12 dargestellten Peptids, T-Zellen immunologisch zu stimulieren, imitiert;

c)

NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>-COOH (SEQ ID NO 53),

LMGYIPLVGAPLGGGAARALA (SEQ ID NO 11 = Peptid CORE 23),

NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 62),

NH<sub>2</sub>-X<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 63),

NH<sub>2</sub>-YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 64),

NH<sub>2</sub>-IPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 65),

NH<sub>2</sub>-X<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 66),

NH<sub>2</sub>-X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 68),

LMGYIPLV (SEQ ID NO 69),

MGYIPLV (SEQ ID NO 70),

YIPLVGAPL (SEQ ID NO 71),

IPLVGAPL (SEQ ID NO 72),

LVGAPLGGGA (SEQ ID NO 94) or

VGAPLGGGA (SEQ ID NO 95),

worin das Peptid die Charakteristik des wie in SEQ ID NO 11 dargestellten Peptids, T-Zellen immunologisch zu stimulieren, imitiert;

d)

NH<sub>2</sub>-X<sub>11</sub>X<sub>12</sub>DPRX<sub>13</sub>X<sub>14</sub>SRNX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>TC-COOH (SEQ ID NO 54),

PTDPRRRSRNLGKVIDTLTC (SEQ ID NO 9 = Peptid CORE 19),

NH<sub>2</sub>-NX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 96),

NH<sub>2</sub>-X<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 97),

NLGKVIDTL (SEQ ID NO 98) oder

LGKVIDTL (SEQ ID NO 117),

worin das Peptid die Charakteristik des wie in SEQ ID NO 9 dargestellten Peptids, T-Zellen immunologisch zu stimulieren, imitiert;

e)

NH<sub>2</sub>-GX<sub>1</sub>X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PWPLYX<sub>6</sub>NX<sub>7</sub>GX<sub>8</sub>G-COOH (SEQ ID NO 99),

GRTWAQPGYPWPLYGNEGCG (SEQ ID NO 6 = Peptid CORE 13),

NH<sub>2</sub>-X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 100),

NH<sub>2</sub>-WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 101),

TWAQPGYPW (SEQ ID NO 102) oder

WAQPGYPW (SEQ ID NO 103),

worin das Peptid die Charakteristik des wie in SEQ ID NO 6 dargestellten Peptids, T-Zellen immunologisch

zu stimulieren, imitiert;

worin X<sub>1</sub> für R oder K, X<sub>2</sub> für A, S oder T, X<sub>3</sub> für A oder G, X<sub>4</sub> für Q, K oder R, X<sub>5</sub> für Y oder H, X<sub>6</sub> für G oder A, X<sub>7</sub> für E oder K, X<sub>8</sub> für C, M oder L, X<sub>9</sub> für W oder L, X<sub>10</sub> für S, N, T, D oder H, X<sub>11</sub> für P oder Q, X<sub>12</sub> für N oder T, X<sub>13</sub> für R oder H, X<sub>14</sub> für R oder K, X<sub>15</sub> für L oder V oder F, X<sub>16</sub> für K oder R, X<sub>17</sub> für L oder I, X<sub>18</sub> für F oder L, X<sub>19</sub> für M oder I, X<sub>20</sub> für G oder E, X<sub>21</sub> für L oder V oder I, X<sub>22</sub> für V oder L, X<sub>23</sub> für A oder G, X<sub>24</sub> für L, V oder I, X<sub>25</sub> für A oder V, X<sub>26</sub> für A oder S, X<sub>27</sub> für R oder A, X<sub>28</sub> für A oder T oder E, X<sub>29</sub> für A oder E, X<sub>30</sub> für V oder A oder L, X<sub>31</sub> für L oder V oder I, X<sub>32</sub> für E oder G, X<sub>33</sub> für V oder I, X<sub>34</sub> für F oder Y, X<sub>35</sub> für A oder P und X<sub>36</sub> für L oder I steht.

29. Immunogene Zusammensetzung, bestehend aus bzw. umfassend wenigstens ein mit einem pharmazeutisch unbedenklichen Hilfsstoff vermischtes Peptid oder Polypeptid nach Anspruch 28.

30. Impfstoffzusammensetzung nach Anspruch 29.

31. Prophylaktische Impfstoffzusammensetzung nach Anspruch 30.

32. Therapeutische Impfstoffzusammensetzung nach Anspruch 30.

33. Zusammensetzung nach einem der Ansprüche 29 bis 32, wobei die Zusammensetzung neben einem beliebigen der Polypeptide nach Anspruch 28 ein Peptid oder Polypeptid, das wenigstens ein B-Zellen stimulierendes HCV-Epitop enthält, und/oder ein HCV-Strukturpolypeptid und/oder ein nicht strukturelles HCV-Polypeptid umfaßt.

34. Zusammensetzung nach einem der Ansprüche 29 bis 33, worin das Polypeptid nach Anspruch 28 in mit HBsAg oder HBcAg-Partikeln, HBV-Immunogenen, HIV-Immunogenen und/oder HTLV-Immunogenen vermischter Form vorliegt.

35. Verwendung eines rekombinanten Expressionsvektors, der eine für ein Polypeptid gemäß einem der Ansprüche 1 bis 22 codierende Nukleinsäureinsertion enthält, zur Herstellung einer HCV-immunogenen Zusammensetzung.

## Revendications

1. Utilisation d'un polypeptide d'environ 8 à environ 20 acides aminés pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés à partir de la région comprise entre les positions d'acides aminés 157 à 176 de la région de noyau de HCV :

$\text{NH}_2\text{-X}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{PGCSFSI-COOH}$  (SEQ ID NO 51),

et lesdits acides aminés contigus contenant un épitope stimulant des lymphocytes T, et dans laquelle ledit polypeptide mime les propriétés de stimulation immunologique des lymphocytes T du polypeptide tel que représenté à la SEQ ID NO 13, et dans laquelle X<sub>30</sub> représente V ou A ou L, X<sub>31</sub> représente L ou V ou I, X<sub>32</sub> représente E ou G, X<sub>33</sub> représente V ou I, et X<sub>34</sub> représente F ou Y, X<sub>35</sub> représente A ou P, X<sub>36</sub> représente L ou I.

2. Utilisation suivant la revendication 1, pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés à partir de la région comprise entre les positions d'acides aminés 157 à 176 de la région de noyau de HCV :

VLEDGVNYATGNLPGCSFSI (SEQ ID NO 13 = peptide CORE 27)

ou VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73).

3. Utilisation suivant la revendication 1, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi la liste suivante de peptides :

$\text{NH}_2\text{-GX}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 74),

$\text{NH}_2\text{-X}_{33}\text{NX}_{34}\text{X}_{35}\text{TGNX}_{36}\text{-COOH}$  (SEQ ID NO 75),

$\text{NH}_2\text{-NX}_{36}\text{PGCSFSI}\text{-COOH}$  (SEQ ID NO 76), et

$\text{NH}_2\text{-X}_{36}\text{PGCSFSI}\text{-COOH}$  (SEQ ID NO 77).

4. Utilisation suivant la revendication 1, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi la liste suivante de peptides :

GVNYATGNL (SEQ ID NO 78)

NLPGCSFSI (SEQ ID NO 80) et

LPGCSFSI (SEQ ID NO 81).

5. Utilisation d'un polypeptide d'environ 8 à environ 20 acides aminés pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés parmi la région comprise entre les positions d'acides aminés 145 à 164 de la région de noyau de HCV :  $\text{NH}_2\text{-GGX}_{25}\text{X}_{26}\text{X}_{27}\text{X}_{28}\text{LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 52), et lesdits acides aminés contigus contenant un épitope de stimulant des lymphocytes T, dans laquelle ledit polypeptide mime les propriétés de stimulation immunologique de lymphocytes T du polypeptide tel que représenté à la SEQ ID NO 12, et dans laquelle  $\text{X}_{25}$  représente A ou V,  $\text{X}_{26}$  représente A ou S,  $\text{X}_{27}$  représente R ou A,  $\text{X}_{28}$  représente A ou T ou E,  $\text{X}_{29}$  représente A ou E,  $\text{X}_{30}$  représente V ou A ou L,  $\text{X}_{31}$  représente L ou V ou I,  $\text{X}_{32}$  représente E ou G,  $\text{X}_{33}$  représente V ou I, et  $\text{X}_{34}$  représente F ou Y.

6. Utilisation suivant la revendication 5, pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés parmi la région comprise entre les positions d'acides aminés 145 à 164 de la région de noyau de HCV :

GGAARALAHGVRVLEDGVNY (SEQ ID NO 12 = peptide CORE 25)

ou GGVAARALAHGVRVLEDGVNY (SEQ ID NO 118).

7. Utilisation suivant la revendication 5, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi la liste suivante de peptides :

$\text{NH}_2\text{-X}_{28}\text{LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{-COOH}$  (SEQ ID NO 82),

$\text{NH}_2\text{-LX}_{29}\text{HGVRX}_{30}\text{X}_{31}\text{-COOH}$  (SEQ ID NO 83),

$\text{NH}_2\text{-GVRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{-COOH}$  (SEQ ID NO 84),

$\text{NH}_2\text{-VRX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{-COOH}$  (SEQ ID NO 85),

$\text{NH}_2\text{-RX}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 86), et

$\text{NH}_2\text{-X}_{30}\text{X}_{31}\text{X}_{32}\text{DGX}_{33}\text{NX}_{34}\text{-COOH}$  (SEQ ID NO 87).

8. Utilisation suivant la revendication 5, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi la liste suivante de peptides :

ALAHGVRVL (SEQ ID NO 88),  
 LAHGVRVL (SEQ ID NO 89),  
 5 VRVLEDGV (SEQ ID NO 90),  
 RVLEDGV (SEQ ID NO 91),  
 VLEDGVNY (SEQ ID NO 92), et  
 10 LEDGVNY (SEQ ID NO 93).

- 15 9. Utilisation d'un polypeptide d'environ 8 à environ 20 acides aminés pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés parmi la région comprise entre les positions d'acides aminés 133 à 152 ou la région de noyau de HCV :  $\text{NH}_2\text{-LX}_{19}\text{X}_{20}\text{YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{X}_{26}\text{X}_{27}\text{X}_{28}\text{LX}_{29}\text{-COOH}$  (SEQ ID NO 53), et lesdits acides aminés contigus contenant un épitope stimulant des lymphocytes T, et dans laquelle ledit polypeptide mime les propriétés de stimulation de lymphocytes T du polypeptide tel que représenté à la SEQ ID NO 11 et dans laquelle  $\text{X}_{19}$  représente M ou I,  $\text{X}_{20}$  représente G ou E,  $\text{X}_{21}$  représente L ou V ou I,  $\text{X}_{22}$  représente V ou L,  $\text{X}_{23}$  représente A ou G,  $\text{X}_{24}$  représente L, V ou I,  $\text{X}_{25}$  représente A ou V,  $\text{X}_{26}$  représente A ou S,  $\text{X}_{27}$  représente R ou A,  $\text{X}_{28}$  représente A ou T ou E,  $\text{X}_{29}$  représente A ou E.
- 25 10. Utilisation suivant la revendication 9, pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés parmi la région comprise entre les positions d'acides aminés 133 à 152 de la région de noyau de HCV :

30 LMGYIPLVGAPLGGAARALA (SEQ ID NO 11 = peptide CORE 23).

11. Utilisation suivant la revendication 9, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi la liste suivante de peptides :

35  $\text{NH}_2\text{-LX}_{19}\text{X}_{20}\text{YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}$  (SEQ ID NO 62),

40  $\text{NH}_2\text{-X}_{19}\text{X}_{20}\text{YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}$  (SEQ ID NO 63),

$\text{NH}_2\text{-YIPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{-COOH}$  (SEQ ID NO 64),

45  $\text{NH}_2\text{-IPX}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{-COOH}$  (SEQ ID NO 65),

$\text{NH}_2\text{-X}_{21}\text{X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}$  (SEQ ID NO 66), et

50  $\text{NH}_2\text{-X}_{22}\text{GX}_{23}\text{PX}_{24}\text{GGX}_{25}\text{-COOH}$  (SEQ ID NO 68).

12. Utilisation suivant la revendication 9, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi la liste suivante de peptides :



LMGYIPLV (SEQ ID NO 69),  
 MGYIPLV (SEQ ID NO 70),  
 5 YIPLVGAPL (SEQ ID NO 71),  
 IPLVGAPL (SEQ ID NO 72),  
 LVGAPLGA (SEQ ID NO 94), et  
 10 VGAPLGA (SEQ ID NO 95).

13. Utilisation d'un polypeptide d'environ 8 à environ 20 acides aminés pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés parmi la région comprise entre les positions d'acides aminés 109 à 128 de la région de noyau de HCV :  $\text{NH}_2\text{-X}_{11}\text{X}_{12}\text{DPRX}_{13}\text{X}_{14}\text{SRNX}_{15}\text{GX}_{16}\text{VIDTX}_{17}\text{TC-COOH}$  (SEQ ID NO 54), et lesdits acides aminés contigus contenant un épitope stimulant des lymphocytes T, et dans laquelle ledit polypeptide mime les propriétés de stimulation immunologique de lymphocytes T du polypeptide tel que représenté à la SEQ ID NO 9, et dans laquelle  $\text{X}_{11}$  représente P ou Q,  $\text{X}_{12}$  représente N ou T,  $\text{X}_{13}$  représente R ou H,  $\text{X}_{14}$  représente R ou K,  $\text{X}_{15}$  représente L ou V ou F,  $\text{X}_{16}$  représente K ou R,  $\text{X}_{17}$  représente L ou I.

14. Utilisation suivant la revendication 13, pour la préparation d'une composition immunogène de HCV ledit polypeptide comprenant ou contenant d'environ 8 à environ 20 acides aminés contigus sélectionnés parmi la région comprise entre les positions d'acides aminés 109 à 128 de la région de noyau de HCV :

PTDPRRRSRNLGKVIDTLTC (SEQ ID NO 9 = peptide CORE 19).

15. Utilisation suivant la revendication 13, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi les peptides suivants :

$\text{NH}_2\text{-NX}_{15}\text{GX}_{16}\text{VIDTX}_{17}\text{-COOH}$  (SEQ ID NO 96), et  
 35  $\text{NH}_2\text{-X}_{15}\text{GX}_{16}\text{VIDTX}_{17}\text{-COOH}$  (SEQ ID NO 97).

16. Utilisation suivant la revendication 13, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant choisi parmi les peptides suivants :

NLGKVIDTL (SEQ ID NO 98), et  
 45 LGKVIDTL (SEQ ID NO 117).

17. Utilisation d'un polypeptide d'environ 8 à environ 20 acides aminés pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'au moins 8 à environ 20 acides aminés contigus sélectionnés parmi la région comprise entre les positions d'acides aminés 73 à 92 de la région de noyau de HCV :  $\text{NH}_2\text{-GX}_1\text{X}_2\text{WX}_3\text{X}_4\text{PGX}_5\text{PWPLYX}_6\text{NX}_7\text{GX}_8\text{-COOH}$  (SEQ ID NO 99), et lesdits acides aminés contigus contenant un épitope de stimulant des lymphocytes T, et dans laquelle ledit polypeptide mime les propriétés de stimulation immunologique de lymphocytes T du polypeptide tel que représenté à la SEQ ID NO 6, et dans laquelle  $\text{X}_1$  représente, R ou K,  $\text{X}_2$  représente A, S ou T,  $\text{X}_3$  représente A ou G,  $\text{X}_4$  représente Q, K ou R,  $\text{X}_5$  représente Y ou H,  $\text{X}_6$  représente G ou A,  $\text{X}_7$  représente E ou K, et  $\text{X}_8$  représente C, M ou L.

18. Utilisation suivant la revendication 17, pour la préparation d'une composition immunogène de HCV, ledit polypeptide comprenant ou contenant d'au moins 8 à environ 20 acides aminés contigus sélectionnés parmi la région

comprise entre les positions d'acides aminés 73 à 92 de la région de noyau de HCV :

GRTWAQPGYPWPPLYGNEGCG (SEQ ID NO 6 = peptide CORE 13) .

19. Utilisation suivant la revendication 17, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant sélectionné parmi :

$\text{NH}_2\text{-X}_2\text{WX}_3\text{X}_4\text{PGX}_5\text{PW-COOH}$  (SEQ ID NO 100), et

$\text{NH}_2\text{-WX}_3\text{X}_4\text{PGX}_5\text{PW-COOH}$  (SEQ ID NO 101) :

20. Utilisation suivant la revendication 17, pour la préparation d'une composition immunogène de HCV, ledit polypeptide étant sélectionné parmi :

TWAQPGYPW (SEQ ID NO 102), et

WAQPGYPW (SEQ ID NO 103) .

21. Utilisation suivant l'une quelconque des revendications 1 à 20, dans laquelle ledit épitope de stimulant des lymphocytes T est un épitope de lymphocytes T auxiliaires.

22. Utilisation suivant l'une quelconque des revendications 1 à 20, dans laquelle ledit épitope de stimulant des lymphocytes T est un épitope CTL.

23. Utilisation suivant l'une quelconque des revendications 1 à 22, dans laquelle ledit polypeptide est incorporé dans une composition vaccinale prophylactique.

24. Utilisation suivant l'une quelconque des revendications 1 à 22, dans laquelle ledit polypeptide est incorporé dans une composition vaccinale thérapeutique.

25. Polypeptide comprenant des répétitions multiples, des combinaisons ou des mimotopes d'une quelconque des séquences d'acides aminés contigus sélectionnées pour qu'elles contiennent des épitopes stimulant des lymphocytes T comme défini suivant l'une quelconque des revendications 1 à 22, lesdites combinaisons comprenant deux peptides ou davantage joints en une structure unique et lesdits mimotopes présentant une ou plusieurs variations d'acides aminés en comparaison desdits peptides pour autant que lesdits peptides mimotopes puissent procurer une stimulation immunologique, après quoi les lymphocytes T sont réactifs vis-à-vis d'au moins une souche de HCV.

26. Utilisation suivant l'une quelconque des revendications 1 à 24, ledit polypeptide étant un polypeptide recombinant exprimé à l'aide d'un vecteur d'expression comprenant un insert d'acide nucléique codant pour un polypeptide suivant l'une quelconque des revendications 1 à 22.

27. Utilisation suivant l'une quelconque des revendications 1 à 24, dans laquelle ledit polypeptide est lié de manière fonctionnelle à un immunogène apparenté à un pathogène, tel que les protéines d'enveloppe de HCV E1 et E2, ou les immogènes du HCV NS3, NS4 ou NSS, ou un peptide de HCV contenant un épitope de stimulant des lymphocytes B.

28. Peptide comprenant au moins 8 acides aminés contigus de la séquence d'un quelconque des peptides suivants, lesdits peptides contenant un épitope de lymphocytes T :

a)

NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>PGCSFSI-OOH (SEQ ID NO 51),  
 VLEDGVNYATGNLPGCSFSI (SEQ ID  
 NO 13 = peptide CORE 27),  
 VLEDIVNYATGNLPGCSFSI (SEQ ID NO 73),  
 NH<sub>2</sub>-GX<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>-COOH (SEQ ID NO 74),  
 NH<sub>2</sub>-X<sub>33</sub>NX<sub>34</sub>X<sub>35</sub>TGN-X<sub>36</sub>-COOH (SEQ ID NO 75),  
 NH<sub>2</sub>-NX<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 76),  
 NH<sub>2</sub>-X<sub>36</sub>PGCSFSI-COOH (SEQ ID NO 77),  
 GVNYATGNL (SEQ ID NO 78),  
 NLPGCSFSI (SEQ ID NO 80), ou  
 LPGCSFSI (SEQ ID NO 81),

dans lequel ledit peptide mime les propriétés de stimulation immunologique de lymphocytes T du peptide  
 représenté à la SEQ ID NO 13;

b)

NH<sub>2</sub>-GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID  
 NO 52),  
 GGAARALAHGVRVLEDGVNY (SEQ ID  
 NO 12 = peptide CORE 25),  
 GGVAARALAHGVRVLEDGVNY (SEQ ID NO 118),  
 NH<sub>2</sub>-X<sub>28</sub>LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 82),  
 NH<sub>2</sub>-LX<sub>29</sub>HGVRX<sub>30</sub>X<sub>31</sub>-COOH (SEQ ID NO 83),  
 NH<sub>2</sub>-GVRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 84),  
 NH<sub>2</sub>-VRX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>-COOH (SEQ ID NO 85),  
 NH<sub>2</sub>-RX<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 86),

NH<sub>2</sub>-X<sub>30</sub>X<sub>31</sub>X<sub>32</sub>DGX<sub>33</sub>NX<sub>34</sub>-COOH (SEQ ID NO 87),  
 ALAHGVRVL (SEQ ID NO 88),  
 LAHGVRVL (SEQ ID NO 89),  
 VRVLEDGV (SEQ ID NO 90),  
 RVLEDGV (SEQ ID NO 91),  
 VLEDGVNY (SEQ ID NO 92), ou  
 LEDGVNY (SEQ ID NO 93),

dans lequel ledit peptide mime les propriétés de stimulation immunologique de lymphocytes T du peptide représenté à la SEQ ID NO 12;

C)

5           NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>X<sub>26</sub>X<sub>27</sub>X<sub>28</sub>LX<sub>29</sub>-COOH (SEQ ID  
NO 53),  
10           LMGYIPLVGAPLGGARALA (SEQ ID  
NO 11 = peptide CORE 23),  
          NH<sub>2</sub>-LX<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 62),  
15           NH<sub>2</sub>-X<sub>19</sub>X<sub>20</sub>YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 63),  
          NH<sub>2</sub>-YIPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 64),  
          NH<sub>2</sub>-IPX<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>-COOH (SEQ ID NO 65),  
20           NH<sub>2</sub>-X<sub>21</sub>X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 66),  
          NH<sub>2</sub>-X<sub>22</sub>GX<sub>23</sub>PX<sub>24</sub>GGX<sub>25</sub>-COOH (SEQ ID NO 68),  
          LMGYIPLV (SEQ ID NO 69),  
25           MGYIPLV (SEQ ID NO 70),  
          YIPLVGAPL (SEQ ID NO 71),  
          IPLVGAPL (SEQ ID NO 72),  
30           LVGAPLGGGA (SEQ ID NO 94), ou  
          VGAPLGGGA (SEQ ID NO 95),

35           dans lequel ledit peptide mime les propriétés de stimulation immunologique de lymphocytes T du peptide représenté à la SEQ ID NO 11;

d)

40           NH<sub>2</sub>-X<sub>11</sub>X<sub>12</sub>DPRX<sub>13</sub>X<sub>14</sub>SRNX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>TC-COOH (SEQ ID NO 54),  
          PTDPRRRSRNLGKVIDTLTC (SEQ ID NO 9 = peptide CORE 19),  
          NH<sub>2</sub>-NX<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 96),  
          NH<sub>2</sub>-X<sub>15</sub>GX<sub>16</sub>VIDTX<sub>17</sub>-COOH (SEQ ID NO 97),  
45           NLGKVIDTL (SEQ ID NO 98), ou

          LGKVIDTL (SEQ ID NO 117),

50           dans lequel ledit peptide mime les propriétés de stimulation immunologique de lymphocytes T du peptide tel que représenté à la SEQ ID NO 9;

e)

55

NH<sub>2</sub>-GX<sub>1</sub>X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PWPLYX<sub>6</sub>NX<sub>7</sub>GX<sub>8</sub>G-COOH (SEQ ID NO 99),  
 GRTWAQPGYPWPPLYGNEGCG (SEQ ID NO 6 = peptide CORE 13),  
 5 NH<sub>2</sub>-X<sub>2</sub>WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 100),  
 NH<sub>2</sub>-WX<sub>3</sub>X<sub>4</sub>PGX<sub>5</sub>PW-COOH (SEQ ID NO 101),  
 TWAQPGYPW (SEQ ID NO 102), ou  
 10 WAQPGYPW (SEQ ID NO 103),

dans lequel ledit peptide mime les propriétés de stimulation immunologique de lymphocytes T du peptide tel  
 que représenté à la SEQ ID NO 6;

15 dans lesquelles X<sub>1</sub> représente R ou K, X<sub>2</sub> représente A, S ou T, X<sub>3</sub> représente A ou G, X<sub>4</sub> représente Q, K ou R,  
 X<sub>5</sub> représente Y ou H, X<sub>6</sub> représente G ou A, X<sub>7</sub> représente E ou K, X<sub>8</sub> représente C, M ou L, X<sub>9</sub> représente W ou  
 L, X<sub>10</sub> représente S, N, T, D ou H, X<sub>11</sub> représente P ou Q, X<sub>12</sub> représente N ou T, X<sub>13</sub> représente R ou H, X<sub>14</sub>  
 20 représente R ou K, X<sub>15</sub> représente L ou V ou F, X<sub>16</sub> représente K ou R, X<sub>17</sub> représente L ou I, X<sub>18</sub> représente F  
 ou L, X<sub>19</sub> représente M ou I, X<sub>20</sub> représente G ou E, X<sub>21</sub> représente L ou V ou I, X<sub>22</sub> représente V ou L, X<sub>23</sub>  
 représente A ou G, X<sub>24</sub> représente L, V ou I, X<sub>25</sub> représente A ou V, X<sub>26</sub> représente A ou S, X<sub>27</sub> représente R ou  
 A, X<sub>28</sub> représente A ou T ou E, X<sub>29</sub> représente A ou E, X<sub>30</sub> représente V ou A ou L, X<sub>31</sub> représente L ou V ou I,  
 X<sub>32</sub> représente E ou G, X<sub>33</sub> représente V ou I, X<sub>34</sub> représente F ou Y, X<sub>35</sub> représente A ou P et X<sub>36</sub> représente L ou I.

25 29. Composition immunogène contenant ou comprenant au moins un des peptides ou polypeptides suivant la re-  
 vendication 28 mélangé avec un excipient pharmaceutiquement acceptable.

30. Composition vaccinale suivant la revendication 29.

30 31. Composition vaccinale prophylactique suivant la revendication 30.

32. Composition vaccinale thérapeutique suivant la revendication 30.

35 33. Composition suivant l'une quelconque des revendications 29 à 32, ladite composition comprenant en plus d'un  
 quelconque des polypeptides suivant la revendication 28, un peptide ou un polypeptide contenant au moins un  
 épitope stimulant des lymphocytes B de HCV, et/ou un polypeptide structurel de HCV, et/ou un polypeptide non  
 structurel de HCV.

40 34. Composition suivant l'une quelconque des revendications 29 à 33, dans laquelle ledit polypeptide suivant la re-  
 vendication 28 est mélangé à des particules de HBsAg ou de HBcAg, des immunogènes de HBV, des immuno-  
 gènes de HIV et/ou des immunogènes de HTLV.

45 35. Utilisation d'un vecteur d'expression recombinant comprenant un insert d'acide nucléique codant pour un poly-  
 peptide tel que défini suivant l'une quelconque des revendications 1 à 22 pour la préparation d'une composition  
 immunogène de HCV.

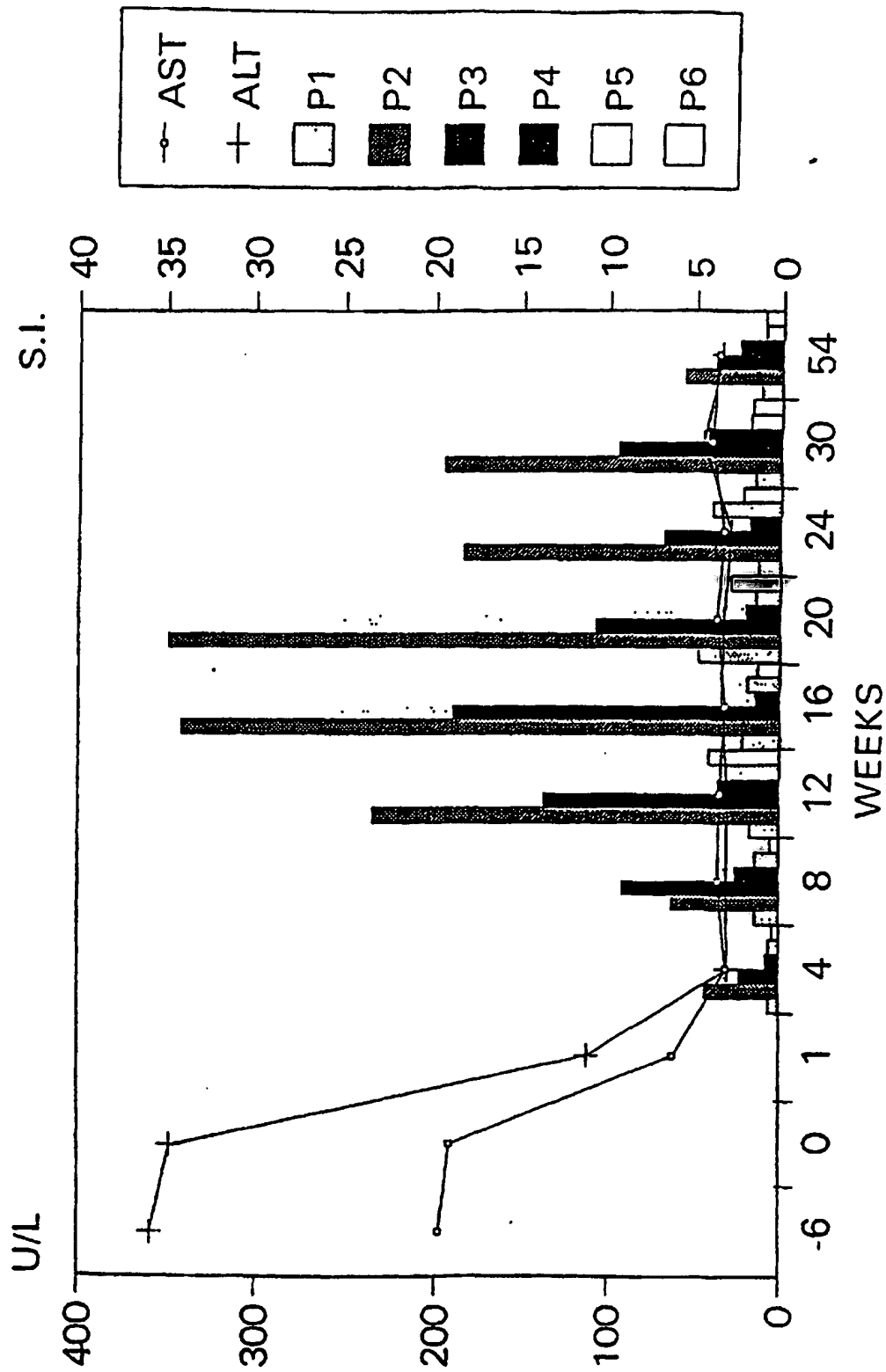


Figure 1. Evolution of lymphoproliferative responses and transaminase activities in HCV patient # 632

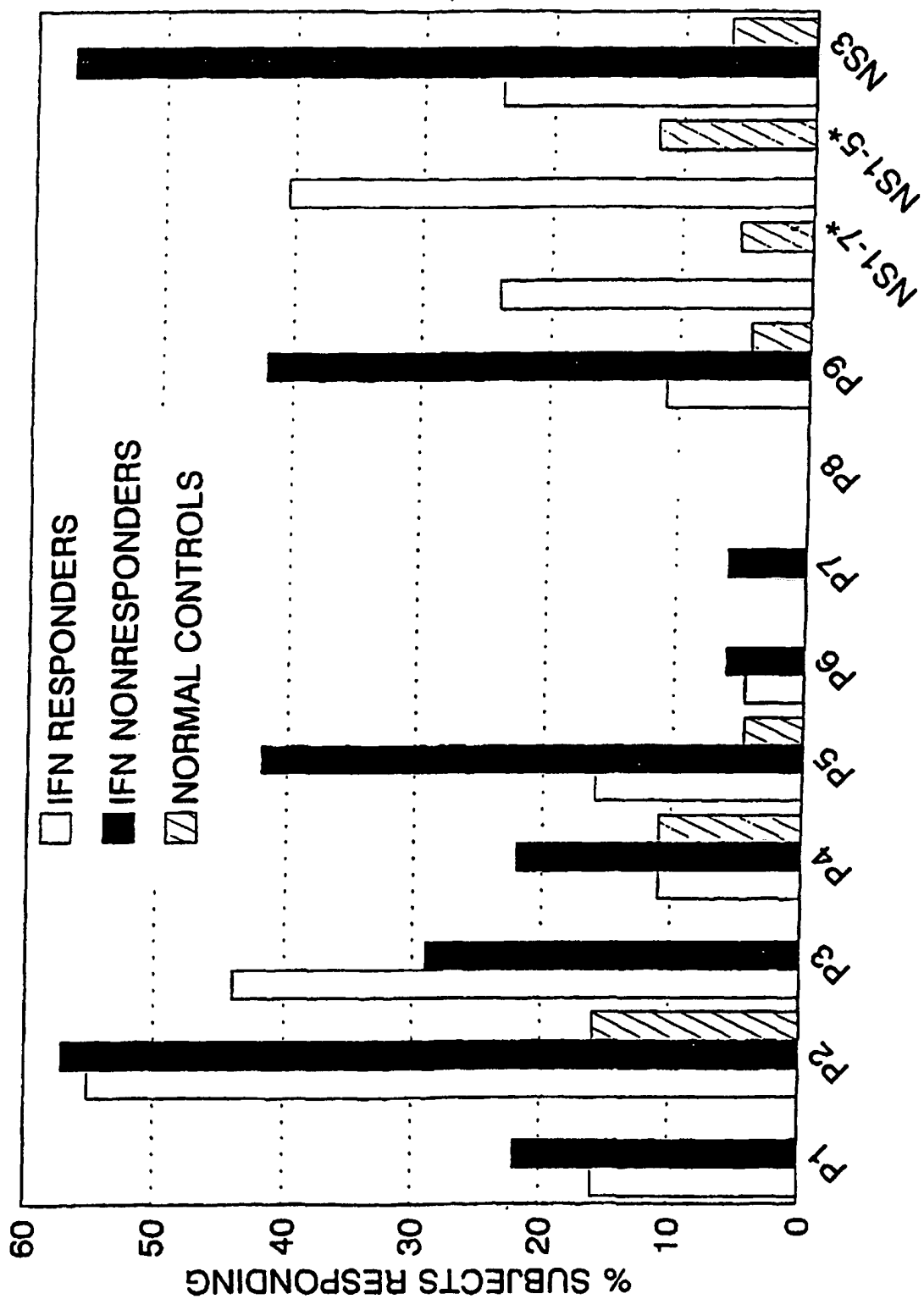


Figure 2

Figure 3

BE8309 NS3 SEQUENCE

GVAKAVDFVPVESMETTMRSPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAA  
QGYKVLVLPNSVAATLGFGAYMSKAHGVDPNIRTGVRTITTGAPITYSTY GKFLADGGC  
SGGAYDIIICDECHSIDSTSI LGIGTVLDQAE TAGARLVVLATATPPGSVTVPHPNIEE  
VALSSTGEIPFYGKAIPIEVIKGGRH LIFCHSKKKCDELA AKLSGFGINAVAYYRGLDV  
SVIPTSGDVVVVATDALMTGTGDFDSVIDCNCVTQTVD FS



	1	50
HCV-H	1a	MSTNPKPQKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRATR
HCV-1	1a	-----
HC-J1	1a	-----
HCVEC1	1a	I-----
HCVHCT18	1a	-----
HCVHCT23	1a	-----
HCVHCT27	1a	-----
HCVTH	1a	-----
HCV-J	1b	-----
HC-J4.83	1b	-----
HC-J4.91	1b	-----
HCV-China	1b	-----
HCV-JTA	1b	Y-----V-T-
HCV-JTB	1b	Y-----V-T-
HCV-BK	1b	-----P-
HCV-JK1	1b	-----
HCV-T	1b	G-----
BNL1	1d	-----
BNL2	1d	-----
CAM1078	1e	-----V-A-
FR2	1f	-----
HC-J6	2a	-----
HC-J8	2b	-----

Figure 4 - Continued 1

CH610	2c	1	50
CH114	2c		
NE92	2d		
BNL3	2e		
FR4	2f		P-
HD10	3a		
BR33	3a		
BR36	3a		
NZL1	3a		
HCVTR	3b		
GB809-4	4a		
GB116	4c		
GB215	4c		
GB358	4c		
GB809	4c		
DK13	4d		
CAM600	4e		
GB809	4e		
CAMG22	4f		
GB549	4g		
GB438	4h		
CAR4/1205	4i		
CAR4/901	4?		



Figure 4 - Continued 3

HCV-H	1a	51	KTSESRQPRGRRQPIPKARRPEGRRTWAQPGYPWPPLYGNEGCGWAGWLLSP	100
HCV-1	1a		-----	
HC-J1	1a		-----V-----	
HVCEC1	1a		-----	
HCVHCT18	1a		-----	
HCVHCT23	1a		-----	
HCVHCT27	1a		-----	
HCVTH	1a		-----	
HCV-J	1b		-----	
HC-J4.83	1b		-----W-----	
HC-J4.91	1b		-----Q-----	
HCV-China	1b		-----	
HCV-JTA	1b		-----	
HCV-JTB	1b		-----	
HCV-BK	1b		-----	
HCV-JK1	1b		-----	
HCV-T	1b		-----W-----	
BNL1	1d		-----	
BNL2	1d		-----D-----	
CAM1078	1e		-----E-----	
FR2	1f		-----	
HC-J6	2a		-----	
HC-J8	2b		-----	

Figure 4 - Continued 4

CH610	2c	51	100
CH114	2c	---	---
NE92	2d	---	---
BNL3	2e	---	---
FR4	2f	---	---
HD10	3a	---	---
BR33	3a	---	---
BR36	3a	---	---
NZL1	3a	---	---
HCVTR	3b	---	---
GB809	4a	---	---
GB116	4c	---	---
GB215	4c	---	---
GB358	4c	---	---
GB809	4c	---	---
DK13	4d	---	---
CAM600	4e	---	---
GB809	4e	---	---
CAMG22	4f	---	---
GB549	4g	---	---
GB438	4h	---	---
CAR4/1205	4i	---	---
CAR4/901	4?	---	---

Figure 4 - Continued 5

BNL7	4k	51	100
BE95	5a	-----S-----S-----X-----	
BE100	5a	-----Q-T-S-G-----A-----L-----	
HK2	6a	-----Q-Q-H-----	
FR1	7a	-----V-Q-T-S-G-----	
VN4	8a	-----V-HQT-----	
VN12	8b	-----A-----V-QNQ-----	
VN13	9a	-----V-HQT-----	
NE98	10a	-----S-----R-----T-----S-----	

Figure 4 - Continued 6

HCV-H	1a	101	150
HCV-1	1a	RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGAARA	
HC-J1	1a	-----	-----
HCVEC1	1a	-----	-----
HCVHCT18	1a	-----	-----
HCVHCT23	1a	-----	-----
HCVHCT27	1a	-----	-----R-----
HCVTH	1a	-----	-----
HCV-J	1b	-----	-----
HC-J4.83	1b	-----	-----
HC-J4.91	1b	-----	-----
HCV-China	1b	-----	-----
HCV-JTA	1b	-----	-----
HCV-JTB	1b	-----	-----
HCV-BK	1b	-----	-----
HCV-JK1	1b	Y-----R-----	-----
HCV-T	1b	-----N-----	-----
BNL1	1d	-----N-----	-----V-----
BNL2	1d	-----	-----
CAM1078	1e	-----	-----
FR2	1f	-----N-----	-----S-T-----
HC-J6	2a	-----N-----H-----V-----	-----V-----
HC-J8	2b	-----T-----H-----R-----I-----	-----V-----V-----

Figure 4 - Continued 7

CH610	2c	101	150
CH114	2c	-----H-----V-----V-----V-----	-----V-----V-----
NE92	2d	-----H-----V-----V-----V-----	-----X-----X-----V-----
BNL3	2e	-----XX-----X-----V-----V-----	-----V-----V-----V-----
FR4	2f	-----N-----H-----X-----V-----V-----	-----V-----V-----V-----
HD10	3a	-----H-----V-----V-----V-----	-----V-----V-----V-----
BR33	3a	-----H-----V-----V-----V-----	-----V-----V-----V-----
BR36	3a	-----H-----V-----V-----V-----	-----V-----V-----V-----
NZL1	3a	-----H-----V-----V-----V-----	-----V-----V-----V-----
HCVTR	3b	-----N-----F-----V-----V-----	-----V-----V-----V-----
GB809_4	4a	-----N-----F-----V-----V-----	-----V-----V-----V-----
GB116	4c	-----N-----F-----V-----V-----	-----V-----V-----V-----
GB215	4c	-----N-----F-----V-----V-----	-----V-----V-----V-----
GB358	4c	-----N-----F-----V-----V-----	-----V-----V-----V-----
GB809	4c	-----N-----F-----V-----V-----	-----V-----V-----V-----
DK13	4d	-----N-----F-----V-----V-----	-----V-----V-----V-----
CAM600	4e	-----X-----N-----X-----V-----V-----	-----V-----V-----V-----
GB809	4e	-----X-----N-----X-----V-----V-----	-----V-----V-----V-----
CAMG22	4f	-----X-----N-----X-----V-----V-----	-----V-----V-----V-----
GB549	4g	-----X-----N-----X-----V-----V-----	-----V-----V-----V-----
GB438	4h	-----X-----N-----X-----V-----V-----	-----V-----V-----V-----
CAR4/1205	4i	-----X-----N-----X-----V-----V-----	-----V-----V-----V-----
CAR4/901	4?	-----X-----N-----X-----V-----V-----	-----V-----V-----V-----



Figure 4 - Continued 8

BNL7	4k	101	150
BE95	5a	-----N-----	
BE100	5a	-----N-----K-----	
HK2	6a	-----H-----N-----	
FR1	7a	-----N-----N-----XXL-----	
VN4	8a	-----N-----N-----	
VN12	8b	-----D-X-N-----X-----	
VN13	9a	-----X-----N-----N-----X-----	
NE98	10a	-----X-----N-----N-----X-----XX-----IE-----N-----	

Figure 4 - Continued 9

HCV-1	1a	151	LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL	200
HCV-H	1a		-----S-	
HC-J1	1a		-----S-	
HVEC1	1a		-----H-	
HCVHCT18	1a		-----S-I	
HCVHCT23	1a		-----L-	
HCVHCT27	1a		-----I-	
HCVTH	1a		-----I-	
HCV-J	1b		-----E--VS-I	
HC-J4.83	1b		-----E--VS-I	
HC-J4.91	1b		-----E--VS-I	
HCV-China1b			-----T--E--VS-I	
HCV-JTA	1b		-----I--AS--	
HCV-JTB	1b		-----I--RS--	
HCV-BK	1b		-----T--E-H-VS-I	
HCV-JK1	1b		-----V-T-E--VS-V	
HCV-T	1b		-----I--E-H-VS-I	
BNL1	1d		-----XT-HE--AS-V	
BNL2	1d		-----F--TT-HE--AS-V	
FR2	1f		-----XG--XXXXX--X--XX--X--T--E-HST-DG	
HC-J6	2a		-----F--I-T-V--AE-K-ISTG	
HC-J8	2b		-----I--V--VE--ISSS	
CH610	2c		-----I--S--V--VE-K-TSTS	

Figure 4 - Continued 10

S83	2C	151	200
CH114	2C	IX-----M-----	VE-KDTGDS
NE92	2d	I-----	XIS--V--X-----TST-
BNL3	2e	I-X-----	I--V-GL--K-TSSS
FR4	2f	I-----	V--V-XVE-K-TSQA
BNL4	2g	I-----	I--V--I--K-NSHF
BNL5	2h	I-----	V--V--V--K-TSTM
BNL6	2i	I-----	V--V--V--K-TSHS
HD10	3a	I-F-----	I--V--V--A-RS-S
BR33	3a	I-F-----	F--IH--ASLEW--TS--
BR36	3a	I-F-----	F--IH--AGLEW--TS--
NZL1	3a	I-F-----	F--IH--ASLEW--TS--
HCV-TR	3b	I-F-----	F--IH--ASLEW--TS--
GB809_4	4a	A-G-----	F--C--GLEYT-TS--
Z4	4a	AV-----	EHY--AS-I
Z1	4b		EHY--AS-I
GB116	4C	AV-----I-----	VHY--AS-V
GB215	4C	AV-----I-----S-----	T--VNY--AS-V
GB358	4C	AV-----I-----Y-----	T--IH--AS-V
Z6	4C	AV-----I-----	T--VNY--AS-I
Z7	4C		VNY--AS-V
DK13	4d	L-----	VNYH-AS-V
CAM600	4e	AV-----I-----	NY--S-V
			T--VNY--AS-I

Figure 4 - Continued 11

GB809	4e	151	----	AV--	I----	200	----	GVNY--	AS-V
CAMG22	4f		----	AV--	I----		----	VHYH--	TS-I
CAMG27	4f		----	AV--	I----		----	VHYH--	TS-I
GB549	4g		----	AV--	I----		----	QHY--	IS-I
GB438	4h		----	AV--	I----		----	QHY--	AS-I
CAR4/12054i			----	A----	I----		----	IHY--	ASDG
CAR4/901	4?		----	AV--	I----		----	QHY--	VS-I
BNL7	4k				I-F--		----	IN--	VS-I
BNL8	4k				I----		----	IN--	TS-I
BNL9	4k				I----		----	IN--	TS-I
BNL10	4k				I----		----	IN--	TS-I
BNL11	4k				I----		----	IN--	TS-I
BNL12	4l				I----		----	IN--	TS-I
GB724	4?				I----		----	IN--	TS-I
BE95	5a				I----		----	IN--	TS-I
BE100	5a				I----		----	IN--	TS-I
SA4	5a				I----		----	IN--	TS-I
HK2	6a				I----		----	IN--	TS-I
FR1	7a				I----		----	IN--	TS-I
VN4	8a				I----		----	IN--	TS-I
VN12	8b				I----		----	IN--	TS-I
NE98	10a				I----		----	IN--	TS-I

Figure 4 - Continued 12

HCV-1	1a	201	250
HCV-H	1a	YHVTNDCPNSSIVYEADAILHTPGCVPCVREGNASRCWVAMTPTVATRD	
HC-J1	1a	-----V-----	
HVEC1	1a	-----H-----V-----	
HCVHCT18	1a	-----H-----V-----	
HCVHCT23	1a	-----A-----D-V-----K-----	
HCVHCT27	1a	-----T-T-S-----K-PVA-----	
HCVTH	1a	-----A-----	
HCV-J	1b	-----S-----M-M-----S-F-----L-----L-A-N	
HC-J4.83	1b	-----S-----M-M-----D-S-----L-----L-A-N	
HC-J4.91	1b	-----S-----V-M-----S-----L-----L-A-N	
HCV-China1b	1b	-----S-----L-M-----S-----L-----L-A-N	
HCV-JTA	1b	-----S-----GM-M-----N-----L-----L-A-N	
HCV-JTB	1b	-----S-----GM-M-----N-V-----L-----L-A-N	
HCV-BK	1b	-----S-A-----L-M-----S-----L-----L-A-N	
HCV-JK1	1b	-----S-----M-M-----S-----L-----L-A-N	
HCV-T	1b	-----S-----M-M-----N-S-----L-----L-A-N	
BNL1	1d	-----S-----I-MDGM-M-Y-----D-HL-----M-L-----L-VKX	
BNL2	1d	-----L-----I-MSGM-A-----N-S-----MXL-----L-VK-	
FR2	1f	-----S-G-----K-I-----X-----I-----I-----PL-----L-A-I	
HC-J6	2a	-----M-----T-D-TWQLQA-V-V-----EKV-T-----IPVS-N-VQQ	
HC-J8	2b	-----YA-----S-N-TWQLT-V-L-----ENDNGTLH-IQV-N-VKH	
CH610	2c	-----M-----S-----WQLEG-V-----EQI-----PVS-N-I-Q	

Figure 4 - Continued 13

S83	2C	-MP----	S-----	WQLEG-V-----	E-TA-V-----	PVA-NL-ISQ	250
CH114	2C	-M-----	S-----	WQLEG-VX-I-----	EWTNTP-----	PVS-X--I-Q	
NE92	2d	-M-----	Q-----	WQLR--V--V-----	E-EK--I-----	IPVS-NI-VSQ	
BNL3	2e	-MA-----	S-N-----	WQLX--V--V-----	ENSSGRFH-----	IPIS-NI-VSK	
FR4	2f	-MA-----	A-D-----	WQLR--V--V-----	E-S--RTF--T--VS-N--	VSR	
BNL4	2g	-MA-----	S-N-----	IWQM-QG-V--V-----	ELQ--K-----	IPV--N--VNQ	
BNL5	2h	-M-----	S-----	WQLK--V--V-----	E-HQ-Q-----	IPV--N--VSQ	
BNL6	2i	-M-----	S-----	WQLEE-V--V-----	EWKD-T-----	IPV--NI-VSQ	
HD10	3a	-VL-----	S-----	-D-V-----	-QD--T-A--TPV-----	V-Y	
BR33	3a	-VL-----	S-----	-D-V-----	-QD--T-T--TPV-----	V-Y	
BR36	3a	-VL-----	S-----	-D-V-----	-QD--T-T--TPV-----	VKY	
NZL1	3a	-VL-----	S-----	-D-V-----	-QD--T-T--TPV-----	V-Y	
HCV-TR	3b	-VL-----	S-G-----	-E-V--L-----	-TT--Q-S--TTVST-----	V-T	
GB809-4	4a	-I-----	-V-----	-TDHH--L-----	-A--V-----	TPV-----AVS	
Z4	4a	-I-----	-V-----	-DHH--L-----	-MT--T-----	TPV-----VAH	
Z1	4b	-I-----	-T-----	-TEHH-M-L-----	-TE-T-----	PL-----APY	
GB116	4C	-I-----	-V-----	-DYH--L--L-----	-V--Q-----	L-----APY	
GB215	4C	-I-----	-V-----	-DHH--L--L-----	-V--Q-----	LS--APY	
GB358	4C	-I-----	-V-----	-TEHH--L--L-----	-V--Q-----	L-----APY	
Z6	4C	-I-----	-V-----	-EHQ--L--L-----	-V--Q-----	L-----VSY	
Z7	4C	-I-----	-M-----	-EHH--L-----	-Q-----	L-----APY	
DK13	4d	-I-----	-V-----	-TDYH--L-----	-K-T-----	SL-----AQH	
CAM600	4e	-I-----	-A-----	-TENH--L-----	-T--Q-----	L-----SPY	

Figure 4 - Continued 14

GB809	4e	201	--I----	A----	TDNH--	L----	KT--	Q----	L----	250	SPY
CAMG22	4f	--L----	F--VHH--	L----			T--	Q----	L----		L-APY
CAMG27	4f	--I----	F--EHH--	L----			T--	Q----	I-L-		L-APH
GB549	4g	----	DHH-M-L-	L----			T--	T----	PL--		APY
GB438	4h	----	DHH-M-L-	L----			T--	V----	IPL--		VPY
CAR4/12054i		-YI----	ENH----	L--I--			KT--	Q----	L----		L-APH
CAR4/901 4?		----	DHH-M-L-	L--I--			T--	V----	SL--		APY
BNL7	4k	-Y----	DHH----	L----				Q----	L----		APY
BNL8	4k	----	DHH----	L----			T--	Q----	L----		APY
BNL9	4k	--I----	DHH----	L----			V--	Q-S-	L----		I-APY
BNL10	4k	----	DHH--AL-	L----			V--	Q----	L----		APY
BNL11	4k	----	F--DHH--	L----			K--	H----	L----		APY
BNL12	4l	----	SDHH----	L----			KT--	T----	L----		API
GB724	4?	--I----	V--TDHH--	L----			T--	V----	TPV--		AVS
BE95	5a	----	DNL----	A----			MT--	V----	QI--		LSAPS
BE100	5a	----	D-L--A--	A----			KD--	V----	QI--		LSAPS
SA4	5a	----	DNL----	A----			QD--	V-K--	QI--		LSAPN
HK2	6a	--L----	L--DAM--	L--L--			VDDR--	T--H-V--	L--IPN		
FR1	7a	--L----	S-N--F--	ETM--	L----		IKA--	E----	LPVS--		L-VPN
VN4	8a	--L----	ETL----	L----			KXX--	Q----	QAS--		L-VPN
VN12	8b	--L----	NGM----	L----			KT--	LTK--	LSAS--		L-VQN
NE98	10a	-M----	S-G----	G-I--	L----		S--	T----	IPVSX--		VKS

Figure 4 - Continued 15

HCV-1	1a	251	GKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSRRHWT	300
HCV-H	1a		---T---	---
HC-J1	1a		---	---H---
HVCEC1	1a		---	---I---
HCVHCT18	1a		---T---	---
HCVHCT23	1a		---T---	---
HCVHCT27	1a		---T---	---I---
HCVTH	1a		N-----	---
HCV-J	1b		R--T---	---I---
HC-J4.83	1b		SSI-T-TI--V--A-A--M--S--	---YE-
HC-J4.91	1b		ASV-T-TI--V--A-AF--M--S--	---E-
HCV-China1b	1b		ASV-T-TI--V--T-AF--M--I--S--	---E-
HCV-JTA	1b		ATI-TATV--V--A-AFS--M--S--	---YE-
HCV-JTB	1b		TSI-T-TI--V--A-AF--M--S--	---YE-
HCV-BK	1b		TSI-T-TI--V--A-AF--M--S--	---YE-
HCV-JK1	1b		VTI-T-TI--V--A-AF--M--S--	---V-
HCV-T	1b		SSI-T-TI--V--A-A--M--S--	---YE-
BNL1	1d		NSV-TATI--V--A-AF--M--S--	---YE-
BNL2	1d		ASV-TXAI--V--XX-F--M--X--A--	---M-H-
FR2	1f		ANV-TAAI--V--T-AFR--M--	---LYH-
HC-J6	2a		ANA-IDEV--V--A-VF--M-I--G--	---TS---
HC-J8	2b		PGALTQG--T--MV-M--	---G-M-AA-M-IV--QH--F
CH610	2c		RGALTRS--T-V-MI-MA-A--V--A-MILS-A-MV--Q--NF	
			PGTLTKG--A-V-VI-M--V--ALMIAA-AVIA--Q--TF	



Figure 4 - Continued 16

S83	251	PGALTKG--A--II-M--V-----V--ALM-AA-VVVV--QH-TF	300
CH114	2c	PGALTKG--A--VI-M-----V--ALMIAA-AVVA--Q--XF	
NE92	2d	PGALTKG--T--TIIA--F-----I-----A-M	
BNL3	2e	PGALTKG--AR--AV-M-----V--A-MIAA-A-IVA-K--YF	
FR4	2f	PGALTRG--A--TI-M-----I-----A-MIAA-VAVV--QY-TF	
BNL4	2g	PGALTRG--T--TI-MV-----I--V--A-MIAA-VVIV--QH-NF	
BNL5	2h	PGALTRG--T--TI-A--V-----F--A-M--S-F-MI--QH-IF	
BNL6	2i	PGAXTKG--T--II-A--F-----	
HD10	3a	VGATTASI--V-M--A-M-----M--A-----A--R--Q--	
BR33	3a	VGATTASI-S-V--A-M-----M--A-----A--R--Q--	
BR36	3a	VGATTASI-S-V--A-M-----M--A-----A--R--Q--	
NZL1	3a	VGATTASI-S-V--A-M-----M--A-----A--R--Q--	
HCV-TR	3b	LGVTTASI-T-V-M--ARQ-----AF-A--A--R--T--	
GB809_4	4a	MDA-LESF--V-M--A--V--V-----GA--M--Q--	
Z4	4a	PGA-LESF--V-M--A--V--V-----GA--M--MI--R--	
Z1	4b	PNA-LESM--V-M--A--M--F-I-----G-----D-R--	
GB116	4c	VGA-LES--S-V--M--A--V--I-----G-----M-S-Q--	
GB215	4c	IGA-VESF--V-MM--A--V--I-----G-----M-S-R--	
GB358	4c	IGA-LES--S-V--M--A--A--I-----G-----M-S-Q--	
Z6	4c	IGA-LDS--V--M--A--V--I-----GA-----M-S-Q--	
Z7	4c	IGA-LESI--V--M--A--V--I-----G-----M-S-Q--	
DK13	4d	LNA-LES--V--M--G-----I--V--G-----M-S-Q--	
CAM600	4e	AGA-LEP--V--M--A--M--I-----GL-----M--Q--	

Figure 4 - Continued 17

GB809	4e	251	VGA-LEP----	V--M--A--V----	GL-----	M--Q----	300
CAMG22	4f		LGA-LESM----	V--M--T-----	GI-----	A--M--R--L----	
CAMG27	4f		IGA-LESM----	V--M--T-----	I-----	M--N--R--L----	
GB549	4g		VGA-LESM----	V--M--A--V----	I-----	M--R-----	
GB438	4h		LGA-L-SV-Q-V--	M--A-----	I--H--G--	A--MVS-Q-----	
CAR4/12054i			LRA-LSS--A-V--	M--A--A--	F--I-----	A--IR--I-E----	
CAR4/901	4?		LGA-L-S-----	V--M--A-----	G-----	M--Q-----	
BNL7	4k		IGA-LES--S-V--	M--A--V----	I--X-XGL--	M--S--R-----	
BNL8	4k		IGA-LES--S-V--	M--A--V----	I-----	M--S--R-----	
BNL9	4k		IGA-LES--S-V--	M--A--V----	I-----	M--S--R-----	
BNL10	4k		TAA-LES--S-V--	M--A--V----	I--X--GL--	M--SXQ-----	
BNL11	4k		IGA-LES--S-V--	VM--A--V----	I-----	M--S--R-----	
BNL12	4l		LSA-LMSV----	V--M--A--S----	G-----	M--Q-----	
GB724	4?		VDA-LESF----	V--M--A-----	V-----	M--Q-----	
BE95	5a		LGAVTAP----	AV-Y-A-G-A--	A--AL--	M--YR--Q-A--	
BE100	5a		FGAVTAP----	AV-Y--G-A--	A--AL--	M--YR--Q-A--	
SA4	5a		LGAVTAP----	AV-Y-A-G-A--	A--A--	M--YR--Q-T--	
HK2	6a		AST--GF----	V--A--A-VV--	S--I-----	L--A-----	
FR1	7a		SSV-IHGF----	V-----	A-AF--	M--I-----	
VN4	8a		AST-V-GF-K-V-	IM--A-AF--	M-----	GL-----	
VN12	8b		ASVSIRGV-E-V-	-----	A-AF--	M-----	
NE98	10a		PCAATAS--T-V-	MM-XA-----	AL--X--G-SWRH-	Q----	

Figure 4 - Continued 18

HCV-1	1a	301	TQGCNCSIYPGHI	350	TQGCNCSIYPGHI
HCV-H	1a		-----N-----		-----A-----V-----M-----
HC-J1	1a		-----		-----A-----
HCV-EC1	1a		-----		-----
HCVHCT18	1a		-----		-----
HCVHCT23	1a		-----		-----
HCVHCT27	1a		-----		-----
HCVTH	1a		-----		-----
HCV-J	1b		-----VS-----		-----VS-----VV-----V-----
HC-J4.83	1b		-----LS-----		-----VS-----VV-----V-----
HC-J4.91	1b		-----VS-----		-----VS-----VV-----V-----
HCV-China1b			-----V-----		-----VS-----VM-----VV-----
HCV-JTA	1b		-----VS-----		-----VS-----VV-----V-----
HCV-JTB	1b		-----VS-----		-----VS-----VV-----V-----
HCV-BK	1b		-----VS-----		-----VS-----VV-----V-----
HCV-JK1	1b		-----L-----		-----VS-----VV-----V-----
HCV-T	1b		-----V-----		-----VS-----VV-----V-----
BNL1	1d		-----		-----
BNL2	1d		-----		-----
FR2	1f		-----S-----XXX		
HC-J6	2a		-----T-----		-----ATMIL-YAM-V-EV-I-I-G-----
HC-J8	2b		-----Q-----		-----LS-----LTMIL-YAA-V-ELV-EI-F-----
CH610	2c		-----X-----		

Figure 4 - Continued 19

S83	2C	301	V-E-----R-----	319
CH114	2C		V-E-----X	
NE92	2d		V-D-----	
BNL3	2e		V-E-----	
FR4	2f		V-E-----X	
BNL4	2g		S-D-----	
BNL5	2h		V-D-----	
BNL6	2i			
HD10	3a		V-T---L---LS---	
BR33	3a		V-T---L---LS---	
BR36	3a		V-T---L---LS---	
NZL1	3a		V-T---L---LS---	
HCV-TR	3b		V-T---VS---	
3B809_4	4a		--D---T---	
Z4	4a		--E---T---	
Z1	4b		--D---VS---	
3B116	4C		--D---A-V---	
3B215	4C		--D---A---G---	
3B358	4C		--D---A-V---	
Z6	4C		--D---A---	
Z7	4C		--D---A-V---	
DK13	4d		--D---T---	
CAM600	4e		--D---T---	

Figure 4 - Continued 20

GB809	4e	301	319
G22	4f	--D-----A-----	
G27	4f	--E-----T-----	
GB549	4g	--E-----	
GB438	4h	--D-----D-----	
CAR4/12054i		--D-----V-----	
BNL7	4k	--D-----S-----XXXX	
BNL8	4k	--D-----	
BNL9	4k	A-D-----	
BNL10	4k	--D-----	
BNL11	4k	--E-----	
BNL12	4l	V-D-----	
CAR4/901	4?	--D-----V-----	
GB724	4?	--D-----T-----	
BE95	5a	V-N-----S-V-----	
BE100	5a	V-D-----S-V--Q--	
SA4	5a	V-D-----S-----	
HK2	6a	V-D-----T-V-----	
FR1	7a	--D-----XNX--V-----	
VN4	8a	V-E-----T-----	
VN12	8b	A-D-----A-----	
NE98	10a	V-D-----	

Figure 4 - Continued 21

HCV-1	1a	351	AHWGVLAGIAYFSMVGNWAKVLVLLFAGVDA	400	ETHVTGGSAGHTVSGF
HCV-H	1a		-----K-----		-----N--R-TA-L
HC-J1	1a		-----		-----I-S--Q-ARAM--L
HCEC1	1a		-----		
HCVHCT18	1a				
HCVHCT23	1a				
HCVHCT27	1a				
HCVTH	1a				
HCV-J	1b		-----L--Y-----I-M-----G		H-----RVASSTQSL
HC-J4.83	1b		-----L--Y-----I-A-----G		--YTS--A-S--T-TL
HC-J4.91	1b		-----L--Y-----I-A-----G		A-YTS--V--R-T---
HCV-China1b	1b		-----L--YA-----I-M-----G		D-YAS--AQ-RSTL--
HCV-JTA	1b		-----L--Y-----I-M-----G		V-YT-----QARHTQSV
HCV-JTB	1b		-----L--Y-----I-M-----G		V-YT-----QARHTQ-V
HCV-BK	1b		-----L--Y-A-----I-M-----G		D-----AQAK-TNRL
HCV-JK1	1b		-----L--Y-----I-M-----G		T-Y-SV-H-SQ-TRRV
HCV-T	1b		-----L--Y-----I-M-----G		S-I-S--TVAR-THSL
BNL1	1d				
BNL2	1d				
FR2	1f				
HC-J6	2a		-----MF-L-----Q-A-----V-I---A-----		Q--TV---TA-NARTL
HC-J8	2b		G-----VF-L-----Q-A-----IAI---V-----		T-YSS-QE--R--A--

Figure 4 - Continued 22

HCV-1	1a	401	VSL	450
HCV-H	1a		LAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWL	AGLFYHHKFNSS
HC-J1	1a		-G--T-----I-----I-----E-----Q-----	
HCVEC1	1a		---FT-----I-----I-----E-----I-Q-----	
HCVHCT18	1a			
HCVHCT23	1a			
HCVHCT27	1a			
HCVTH	1a			
HCV-J	1b		--W-SQ-PS-KI--V-----I-R-----Q-FI-A--A-R--A-	
HC-J4.83	1b		A--FS--S-RI--V-----I-R-----H-F-A--T-R--	
HC-J4.91	1b		T--FSS--S-KI--V-----I-R-----H-F-A--T--	
HCV-China1b	1b		T--FT--S-KI-----I-R-----F-A--T-R--A-	
HCV-JTA	1b		T-FFTQ-PA-RI-----I-R-----E--FF-A--A--	
HCV-JTB	1b		A-FFT--PA-KI-----I-R-----E--FF-A--A--	
HCV-BK	1b		--MF-S-PS-KI-----I-R-----Q-F-A--T-S--	
HCV-JK1	1b		A-FFS--SA-KI--V-----I-R-----E-I--FF-A--VK--	
HCV-T	1b		A--FTQ--S-KI-----I-R-----Q-F--S--A-R--A-	
BNL1	1d			
BNL2	1d			
FR2	1f			
HC-J6	2a		TGMFSL--R-KI-----I-R-----H-F--S--T-S--	
HC-J8	2b		AG-FTT-----LY-----I-R-----Q-F--S--T--	

Figure 5

HCV-1	571	IGGAGNNT	LHCPTDCFRKHPDATYSRCGSGP
HCV-H	---	V----	-L-----Y-E-----
HC-J1	---	G----	-----E-----
HCV-J	---	V----	-V-----E---TK----
HC-J4.83	---	V--H-	-T-----E---TK----
HC-J4.91	---	V--R-	-I-----E---TK----
HCV-CHINA	---	V----	-T-----E---T-----
HCV-JTA	---	V--L-	-T-----E---TK----
HCV-JTB	---	V--L-	-T-----E---TK----
HCV-BK	---	V----	-T-----E---TK----
HCV-JK1	---	-----	-T-----E---TK----
HCV-T	---	G----	-V-----E---TK----
HC-G9	---	S----	-L-----
HC-J6	---	RADF-ASMD-L-	-----T---IK----
HC-J8	---	RKDY-S-ID-L-	-----LK---A---



Figure 5 continued 1

HCV-1	604	WITPRCLVDYPYRLWHPCTINYTIKIRMYVGGVEH
HCV-H		R-----M-----V-----
HC-J1		-----V-----
HCV-J		-L-----M-----V-F-V-----
HC-J4.83		-L-----F-FS-----V-----
HC-J4.91		-L-----L-FS-----V-----
HCV-CHINA		-L-----V-FA-----V-----
HCV-JTA		-L-----I-----V-F-----V-----
HCV-JTB		-L-----I-----V-F-----V-----
HCV-BK		-L-----M-----V-F-----V-----
HCV-JK1		-L-----M-----F-F-----V-----
HCV-T		-L-----M-----V-F-----V-----
HC-G9		-L-----V-----F-----
HC-J6		-L-----I-----V-----V-----
HC-J8		-L-----V-F-----A-----

	1188	1200
HCV-1	GVAKAVDFIPVEN	
HCV-H	-----	
HC-J1	-----S	
HC3-J	-----S	
BE8309	-----V--S	
HC-J4.83	-----S	
HC-J4.91	-----S	
HCV-CHINA	-----T	
HCV-JTA	-----S	
HCV-JTB	-----S	
HCV-BK	-----V--S	
HCV-JK1	-----S	
HCV-T	-----V--S	
HC-J6	---SI---T	
HC-J8	---SI---S	

	1201	1250
HCV-1	LETTMRSPVFTDNSSPPVVPQSFOVAHLHAPTSGSKSTKVPAAAYAAQGYK	
HCV-H	-----A-----K--	
HC-J1	-----A-----	
HCV-J	M-----A--T-----	
BE8309	M-----A--T-----	
HC-J4.83	M-----A--T-----	
HC-J4.91	M-----A--T-----	
HCV-CHINA	M-----A--T-----	
HCV-JTA	M-----A--T-----	
HCV-JTB	M-----A--T-----X--	
HCV-BK	M-----A-----	
HCV-JK1	M-----A--T-----	
HCV-T	M-----A--A-----	
HC-J6	-DIVT---T-S---T--A---TY--GY-----V-----	
HC-J8	-DVAT-T-S-S---T--A---Y--GY-----S-----	

	1251	1300
HCV-1	VLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFL	
HCV-H	-----V-----	
HC-J1	-----	
HCV-J	-----E-----G-----C--	
BE8309	-----V-----A-----	
HC-J4.83	-----P-----G-----	
HC-J4.91	-----GS-----	
HCV-CHINA	-----V-----A-----	
HCV-JTA	-----T-----A-----	
HCV-JTB	-----T-----G-----	
HCV-BK	-----A-V-----	
HCV-JK1	-----V--S-----A-----	
HCV-T	-----V-----A-----	
HC-J6	-----L-----N-----V--A-----	
HC-J8	-----N-----V--DS-----I	

Figure 6

	1301		1350
HCV-1	ADGGCSGGAYDIIICDECHSTDATSI LGIGTVLDQAETAGARLVVLATAT		
HCV-H	--A-----S-----		
HC-J1	-----V-----		
HCV-J	-----S-T-----		
BE8309	-----I-S-----		
HC-J4.83	-----S-T-----		
HC-J4.91	-----S-T-----		
HCV-CHINA	-----S-T-----		
HCV-JTA	-----S-T-----		
HCV-JTB	-----S-T-----		
HCV-BK	-----S-T-----		
HCV-JK1	-----S-----A-		
HCV-T	-----M-----S-T-----		
HC-J6	---A-----AV-S-T-----V-T---		
HC-J8	---AA-----V-T-----V-----		
	1351		1400
HCV-1	PPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHILFCCHSKKCC		
HCV-H	-----S-----		
HC-J1	---I---A-----A-----		
HCV-J	---I-----N-----I-A-----		
BE8309	-----S-----I-----		
HC-J4.83	-----IG--NN-----I-A-----		
HC-J4.91	-----IG--NN-----I-A-----		
HCV-CHINA	-----N-----I-A-R-----		
HCV-JTA	-----N-----A-----		
HCV-JTB	-----N-----I-----		
HCV-BK	-----N-----I-A-R-----		
HCV-JK1	-----PN-----T-----		
HCV-T	-----I--N-----I-T-----		
HC-J6	---T-----GQE-----R---SY-----		
HC-J8	---T-T-S-----GHE-----AF-----		
	1401		1450
HCV-1	DELAACLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS		
HCV-H	-----S-----F-----		
HC-J1	-----V-----		
HCV-J	-----TG--L-----F-----		
BE8309	-----SGF-----F-----		
HC-J4.83	-----TG--L-----PI--A-----F-----		
HC-J4.91	-----TG--L-----PI-----F-----		
HCV-CHINA	-----SS--L-----S-----F-----		
HCV-JTA	-----SG-----I-----		
HCV-JTB	-----SG-----I-----		
HCV-BK	-----SG-----I-----		
HCV-JK1	-----S--V-----F-----		
HCV-T	-----S--H-----A--N-----F-----		
HC-J6	---A-RGM-L-----Q-----F-----		
HC-J8	---A-RGM-V-----Q-----		

Figure 6 - continued 1

	1451	1465
HCV-1	VIDCNTCVTQTVDFS	
HCV-H	-----	
HC-J1	-----	
HCV-J	-----	
BE8309	-----	
HC-J4.83	-----	
HC-J4.91	-----	
HCV-CHINA	-----	
HCV-JTA	-----	
HCV-JTB	-----	
HCV-BK	-----	
HCV-JK1	-----	
HCV-T	-----	
HC-J6	-----VA---V----	
HC-J8	-----VA-S-I----	

Figure 6 - continued 2